

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:46:29 ; Search time 61 Seconds
(without alignments)
2903.075 Million cell updates/sec

Title: US-09-673-707-1
Perfect score: 1347
Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYGASSYFGQGTKLERK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	828.5	61.5	244	2	Q65ZC8_HUMAN
2	726.5	53.9	240	2	Q65ZC9_HUMAN
3	719.5	53.4	243	2	Q7TQM2_MOUSE
4	703.5	52.2	241	2	Q921A6_MOUSE
5	703.5	52.2	255	2	Q6KB05_MOUSE
6	692.5	51.4	487	2	Q65ZL2_MOUSE
7	658	48.8	248	2	Q92ZQ7_MOUSE
8	597	44.3	218	2	Q925S1_MOUSE
9	436.5	32.4	170	2	Q925S2_MOUSE
10	435	32.3	129	1	KV3L_HUMAN
11	434	32.2	129	1	KV3M_HUMAN
12	431	32.0	518	2	Q6N030_HUMAN
13	427	31.7	109	1	KV3B_HUMAN
14	426	31.6	109	1	KV3E_HUMAN
15	424	31.5	109	1	KV3D_HUMAN
16	422	31.3	108	1	KV3A_HUMAN
17	422	31.3	109	2	Q9UL78_HUMAN
18	421.5	31.3	236	2	Q6PJF8_HUMAN
19	419.5	31.1	500	2	Q9BRV0_HUMAN
20	417.5	31.0	159	2	Q96Q50_HUMAN
21	417	31.0	109	2	Q9UL86_HUMAN
22	414	30.7	480	2	Q6P089_HUMAN
23	410.5	30.5	235	2	Q6PJF2_HUMAN
24	410.5	30.5	236	2	Q6P558_HUMAN
25	410.5	30.5	498	2	Q6N041_HUMAN
26	408	30.3	469	2	Q7Z7P5_HUMAN
27	406	30.1	109	1	KV3G_HUMAN
28	406	30.1	119	2	Q9GY22_MOUSE
29	406	30.1	235	2	Q6GMV9_HUMAN
30	405	30.1	119	2	Q9UL94_HUMAN
31	404	30.0	125	2	Q9UL95_HUMAN

32	403	29.9	500	2	Q6N091_HUMAN	Q6N091	homo sapien
33	400.5	29.7	128	1	KV3K_HUMAN	P06311	homo sapien
34	400.5	29.7	147	1	HV1C_HUMAN	P01744	homo sapien
35	397	29.5	475	2	Q6N055_HUMAN	Q6N055	homo sapien
36	395.5	29.4	124	2	Q9UL92_HUMAN	Q9UL92	homo sapien
37	392.5	29.1	234	2	Q56919_HUMAN	Q56919	homo sapien
38	392	29.1	497	2	Q8WY24_HUMAN	Q8WY24	homo sapien
39	389.5	28.9	613	2	Q8VCX7_MOUSE	Q8VCX7	mus musculus
40	385.5	28.6	168	2	Q8VDC9_MOUSE	Q8VDC9	mus musculus
41	385	28.6	465	2	Q6PJB2_MOUSE	Q6PJB2	mus musculus
42	383.5	28.5	468	2	Q505N9_MOUSE	Q505N9	mus musculus
43	382.5	28.4	480	2	Q6PJF1_HUMAN	Q6PJF1	homo sapien
44	381	28.3	100	1	KV3C_HUMAN	P01621	homo sapien
45	380.5	28.2	617	2	Q4KML5_MOUSE	Q4KML5	mus musculus

ALIGNMENTS

RESULT 1

Q65ZC8_HUMAN

ID Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.

AC Q65ZC8;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Single-chain Fv (Fragment).

GN Name=scFv;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;

RA Kontermann R.E., Wing M.G., Winter G.;

RT "Complement recruitment using bispecific diabodies.";

RL Nat. Biotechnol. 15:629-631(1997).

DR EMBL; Y13057; CAA73500.1; -; mRNA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IG; 2.

DR SMART; SM00406; IGv; 2.

DR PROSITE; PS00835; IG-LIKE; 2.

FT NON_TER 1

FT NON_TER 244

SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 61.5%; Score 828.5; DB 2; Length 244;

Best Local Similarity 64.8%; Pred. No. 1e-57; Indels 7; Gaps 2;

Matches 162; Conservative 26; Mismatches 55;

Qy 2 QVQLQSGAEVKKPGASVKVSQASGYRFSNFTVHWVRQAPGQRFQFWGWINPYNGNKEF 61

Db 1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSIDHYHWVRQAPGQGLEWGWIDPNDGTRF 60

Qy 62 SAKPQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGEWGWDDSPQDNYMDVWGK 121

Db 61 AQRFGQGRVTMTDTSISAAAYMEVSRSLRSDDTAVVYCAREG-----TGSATYGMVWGQ 114

Qy 122 TTVTVSSGGSGSGSGGGSDIELTQSPGTLSPGERATFSCRSHSRISRRAVYQ 181

Db 115 TLTVTVSSGGSGSGGGGGGGSDIQMTQSPSTLSASIGDRVITTCRASEGI-YHWLAWYQ 173

Qy 182 HKPQAPRLVHGVSNRASGISDRFSGSGSGTDFTLITRVPEPDFALYICQVYGCASSYT 241

Db 174 QKGGKAPKFLIYKASSLASGAPSRFSGSGSGTDFTLTIISSLPQDFATYICQIYSNYPLT 233

Qy 242 FGQGTKLERK 251

Db 234 FGGGTKLEIK 243

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RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=Balb/C;
RC      MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA      Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT      "scFv single chain antibody variable fragment as inverse agonist for
RL      the beta-2 adrenergic receptor.";
DR      J. Biol. Chem. 278:36740-36747(2003).
DR      EMBL; AJ574851; CAE00495.1; -; Genomic_DNA.
DR      HSSP; P01751; 1A6W.
DR      SMR; Q7TQM2; 1-236.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      SMART; SM00406; IGV; 2.
DR      PROSITE; PS50835; IG_LIKE; 2.
FT      NON_TER 1
SQ      SEQUENCE 243 AA; 25976 MW; BEPFF64D2DCF4F76 CRC64;

Query Match 53.4%; Score 719.5; DB 2; Length 243;
Best Local Similarity 56.0%; Pred. No. 4.4e-49;
Matches 140; Conservative 41; Mismatches 56; Indels 13; Gaps 3;

QY      2 QVQLQSGAEVKKPGASVKVSQCOASGYRFSNFTVHWVROAPGQRFWMGMINPVGNGKEF 61
DB      1 QVQLQSGSELVRLPGASVKLSCKASGYTFTYMHVWKQRHGQGLEWIGNIYFGSGITNY 60
QY      62 SAKFDQRTVFTADTSANTAYMELRLSADTAVYVCARVGEWGMDDSPQDNYMDVWVGK 121
DB      61 DEKFKNGKILTVDTSSSTAYMHLSSLASEDSAVVYCARGRG-----LDVWGAG 109
QY      122 TTVIVSSGGSGGGGGGGGSDIELTQSPGTLSPGERATFSCRSHSIRSRVAVYQ 181
DB      110 TLTIVSSGGSGGGGGGGGSDIQMTQSSSFVSLGDRVTITCKASDIYN-RLAWYQ 168
QY      182 HKPQAPRLVIHGVNRSAGISDRFSGSGGTDTLTITRVEPEDEALYICQVYGASST 241
DB      169 QKPGNAPRLISATSLTGVPSRFSGSGGKDTLTSLTQIEDVATYICQYW-STRT 227
QY      242 FGQGTGLERK 251
DB      228 FGGGTGLEIK 237

RESULT 4
Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
AC      Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Anti-CEA 79 single chain Fv (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      MEDLINE=98170165; PubMed=9509426;
RA      Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RT      Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RL      "Cloning and characterization of cDNAs encoding VH and VL of a
RT      monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT      generation of a single-chain Fv molecule (scFv).";
RL      Mol. Cells 7:816-819(1997).
[2]
RN      NUCLEOTIDE SEQUENCE.
RP      MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA      Stark S.E., Caton A.J.;
RT      "Antibodies that are specific for a single amino acid interchange in a
RT      protein epitope use structurally distinct variable regions.";
RL      J. Exp. Med. 174:613-624(1991).
DR      EMBL; U88067; AAB48044.1; -; mRNA.

RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=C1q/7;
RC      MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA      Kontermann R.E., Wang M.G., Winter G.;
RT      "Complement recruitment using bispecific diabodies.";
RL      Nat. Biotechnol. 15:629-631(1997).
DR      EMBL; Y13056; CAA73499.1; -; mRNA.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      SMART; SM00409; IG; 2.
DR      SMART; SM00406; IGV; 2.
DR      PROSITE; PS50835; IG_LIKE; 2.
FT      NON_TER 1
SQ      SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;

Query Match 53.9%; Score 726.5; DB 2; Length 240;
Best Local Similarity 56.8%; Pred. No. 1.2e-49;
Matches 142; Conservative 36; Mismatches 61; Indels 11; Gaps 3;

QY      2 QVQLQSGAEVKKPGASVKVSQCOASGYRFSNFTVHWVROAPGQRFWMGMINPVGNGKEF 61
DB      1 QVQLVQSGGLVQPQGGSLRLSCAASGFTFSYGMHWVROAPGKGLWVAIVISYDGSNKY 60
QY      62 SAKFDQRTVFTADTSANTAYMELRLSADTAVYVCARVGEWGMDDSPQDNYMDVWVGK 121
DB      61 ADSVKGRFTISRDNKNTLVLMNSLRAEDTAVYYCAR-----DWGDS----LDPWGK 110
QY      122 TTVIVSSGGSGGGGGGGGSDIELTQSPGTLSPGERATFSCRSHSIRSRVAVYQ 181
DB      111 TLTIVSSGGSGGGGGGGGSDIQMTQSPGTLSPGDRVTITCRASEGI-YRWLAWYQ 169
QY      182 HKPQAPRLVIHGVNRSAGISDRFSGSGGTDTLTITRVEPEDEALYICQVYGASST 241
DB      170 QKPGAPKLLIYKASSLASRAPSRFSGSGGTDTLTITSLQPDPAFYICQYVSNPLT 229
QY      242 FGQGTGLERK 251
DB      230 FGGGTGLEIK 239

RESULT 3
Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
AC      Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      ScFv 6H8 protein (Fragment).
OS      Name=scFv; 6H8.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
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DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSP; P01607; 1BW.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match
Best Local Similarity 52.2%; Score 703.5; DB 2; Length 241;
Matches 136; Conservative 46; Mismatches 52; Indels 21; Gaps 6;

QY 2 QVLEQSGAEVKKPKASVKVSCQASGYRFSNFTVHVWVROAPGQRFWMGWINPYNGNKEF 61
Db 1 QVQLQQSGPELKKPGETVKISKASGYTFTDYGNNVWVKAQPGKGLKMWGINTYTGPTY 60
QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNY-YNDVWGK 120
Db 61 ADFFKGRFAFSLTSASTAYLQINLNKNEIDATYFCAR-----KDLLRFYDWGQ 110
QY 121 GTTVIVSSGGSGGGSGGGSGGGSDIELTQSPOTLSLSPGERATFSCRSRSHSIRRRVAVY 180
Db 111 GTTVIVSSGGSGGGSGGGSGGGSDIELTQSPSSLSASLGKVTITCKASQDI-NKYIANY 169
QY 181 QHKFGQAPR----LVHGVSNRAGISDRFSGSGSGTDFTLTIITRVEPEDFALYYCQVYG 236
Db 170 QHKPGKGRSAHTLHY----IQGIPSRFSGSGSGRDRYSFISNLEPEDIATYCYLHYD 225
QY 237 ASSYTFGGQTKLERK 251
Db 226 -NLHTFGGQTKLELK 239

RESULT 5
Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RL monoclonal anti-M2 receptor antibody fragments."
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 255 AA; 27445 MW; B68BD3895DF713B CRC64;

Query Match
Best Local Similarity 52.2%; Score 703.5; DB 2; Length 255;
Matches 136; Conservative 46; Mismatches 52; Indels 21; Gaps 6;
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Best Local Similarity 52.9%; Pred. No. 8.7e-48;
Matches 135; Conservative 42; Mismatches 67; Indels 11; Gaps 2;

QY 2 QVLEQSGAEVKKPKASVKVSCQASGYRFSNFTVHVWVROAPGQRFWMGWINPYNGNKEF 61
Db 1 QVQLQQSGDLVKPGSLKVSAAASGFTFSSYGMWVRQTPDKRLLEWVATITSGGSYTY 60
QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 121
Db 61 PDSVKGRTISRDNKNTLYLQMSLSKSDTAMVYCARHINYRDGA-----FDYWGQ 114
QY 122 TTVIVSSGGSGGGSGGGSGGGSDIELTQSPOTLSLSPGERATFSCRSRSHSIRSR- 176
Db 115 TTLTVSSGGSGGGSGGGSGGGSDIVMAQSPSSLSVSAKEKVMSCSKSLNSRNQNY 174
QY 177 VAWYQHKGPAQPLRVHGVSNRAGISDRFSGSGSGTDFTLTIITRVEPEDFALYYCQVYG 236
Db 175 LAWYQKPGQSPKLLIYGASTRESGVDPDRFTFGSGSGTDFTLTISSVQAEDLAVYYCONDH 234
QY 237 ASSYTFGGQTKLERK 251
Db 235 SYPLTFGAGTKLEIK 249

RESULT 6
Q65ZL2_9MURI PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE FV/M4.
GN Name=M4-IFN- $\tau$ and>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RL antibody secreted from myeloma cells."
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00408; IGc2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match
Best Local Similarity 51.4%; Score 692.5; DB 2; Length 487;
Matches 131; Conservative 48; Mismatches 56; Indels 15; Gaps 4;

QY 2 QVLEQSGAEVKKPKASVKVSCQASGYRFSNFTVHVWVROAPGQRFWMGWINPYNGNKEF 61
Db 20 QVQLQQSDAEIVKPGASVKISKASGYTFTDTHAIHWAKRQPEQGLEWIGYISPDNDIKY 79
QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 121
Db 80 NERFKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCKR-----SYI-GHWGQ 126
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAUB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
RA Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after gamma-irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAUB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL: AF240167; AAK43732.1; -, mRNA.
DR HSP; P01751; 1AGW.
DR SMR; Q92582; 3-124.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 32.4%; Score 436.5; DB 2; Length 170;
Best Local Similarity 52.9%; Pred. No. 8.3e-27;
Matches 82; Conservative 26; Mismatches 38; Indels 9; Gaps 2;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVQAPGQRFPMWGINPYNGNKEF 61
Db 3 QVQLQQSGPEVVRPGVSKISCKGSGYFTDYSMHLKWNHAQSLIEWIGIISTYDGNTRY 62

Qy 62 SAKQDRVTFADTSANTAYNELSLRSADTAVYICARVGEWDDSPQDNYMDVWCKG 121
Db 63 NQKFGKATMTVDKSSITAYNELARLTSDSAIYICARGAYYG-----SFYFDYWGQG 116

Qy 122 TTVTVSSGGGGGGGGGGGGSDIELTQSPGTL 156
Db 117 TTVTVSSGGGGGGGGGGGGSGGSGE---SSSPGGL 148

RESULT 10
KV3L HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC PIR; P10022; K3HUHA.
DR HSP; P01625; 1EEQ.
DR SMR; P18135; 21-129.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 Jk1 segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match 32.3%; Score 435; DB 1; Length 129;
Best Local Similarity 75.9%; Pred. No. 7.9e-27;
Matches 82; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy 144 DIELTQSPGTLSPGERATFSCRSRHSIRRRVAVYQHKGQAPRLVIHGVSNRASGIS 203
Db 21 EIVLTQSPGTLSPGERATLSCASQSVSSYLAWYQKPGAPRLIYGASSRATGIP 80

Qy 204 DRFGSGSGTDFTLTITRVEPEDFALYYCQVYGASSYTFGGTKLERK 251
Db 81 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYGTSPRTFGGQTKVEIK 128

RESULT 11
KV3M HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; P10021; K3HUHI.
DR HSP; P01625; 1EEQ.
DR SMR; P18136; 21-129.

DR	Ensembl; ENSG00000169769; Homo sapiens.	
DR	GO; GO:0005576; C:extracellular region; NAS.	
DR	GO; GO:0003823; F:antigen binding; NAS.	
DR	GO; GO:0006955; P:immune response; NAS.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	SMART; SM00406; IGv; 1.	
DR	PROSITE; PS50835; IG LIKE; 1.	
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.	
FT	SIGNAL	1 20
FT	CHAIN	21 129
FT	REGION	21 43
FT	REGION	44 55
FT	REGION	56 70
FT	REGION	71 77
FT	REGION	78 109
FT	REGION	110 118
FT	REGION	119 129
FT	DISULFID	43 109
FT	NON_TER	129 129
FT	SEQUENCE	129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;
DR	Query Match	32.2%; Score 434; DB 1; Length 129;
DR	Best Local Similarity	75.0%; Pred. No. 9.5e-27;
DR	Matches	81; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY	144 DIETQSPGTLSPGGERATFSCRSRSHIRRRVAVYQHKPGQAPRLVIHGVNRSAGIS 203	
DB	21 EIVLTQSPGTLSPGGERATLSCRASQSVSSVSLAWYQQKPGAPRLIIYGASRRATGIP 80	
QY	204 DRFGSGSGTDFTLTIITRVEPEDPALYVCQVYGASSYTFGGTKLERK 251	
DB	81 DRFGSGSGTDFTLTIISRLPEXDFAVYCCQYGSSPWFQGGTKVEIK 128	
DR	RESULT 12	
Q6N030 HUMAN		
ID	Q6N030 HUMAN PRELIMINARY; PRT; 518 AA.	
AC	Q6N030;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DE	Hypothetical protein DRFZp686115212.	
GN	Name=DRFZp686115212;	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Rectum tumor;	
RG	The German cDNA Consortium;	
RA	Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,	
RA	Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;	
RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BX640724; CAE45841.1; -, mRNA.	
DR	HSSP; P01861; IADQ.	
DR	InterPro; IPR000005; HTHArac.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig cl.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF07654; C1-set; 3.	
DR	SMART; SM00409; IG; 3.	
DR	SMART; SM00407; IGcl; 3.	
DR	SMART; SM00406; IGv; 1.	
DR	PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.	
DR	PROSITE; PS50835; IG LIKE; 4.	
DR	PROSITE; PS00290; IG MHC; UNKNOWN_2.	
KW	Hypothetical protein.	
QY	SEQUENCE 518 AA; 57019 MW; 9385F98613BF6382 CRC64;	

Query Match	32.0%; Score 431; DB 2; Length 518;	
Best Local Similarity	54.9%; Pred. No. 8.1e-26;	
Matches	90; Conservative 12; Mismatches 36; Indels 26; Gaps 3;	
QY	2 QVQLSOSGAEVKKPKGASVKVSCQASGYRFSNFTVHVVRQAPGQRFQFWMGWINFYNGNKEF 61	
DB	20 QVHLVQSGAEVKKPGASVKVSCASGYRFPFTNFHINVRQAPQGSLEWMGWINTGNGNTKY 79	
QY	62 SAKFQDRVTFTADTSANTAYMELRSADTAVVYCARVGEWGWDDSPQ--DNYYYMDVWG 119	
DB	80 SQKFGQRVITRDYTTWTTAYMDLSLSRSEDYAVVWCAR-----DAQGVGTTTTFYDWG 132	
QY	120 KGTFTIVSSGGSGGGGGGGGGGSDIELTQSPGTLSPGERAT 163	
DB	133 QGTLTVTSAS-----TKGPSVFFPLAPCSRST 159	
DR	RESULT 13	
KV3B HUMAN		
ID	KV3B HUMAN STANDARD; PRT; 109 AA.	
AC	P01620;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	10-MAY-2005 (Rel. 47, Last annotation update)	
DE	Ig kappa chain V-III region SIE.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	PROTEIN SEQUENCE.	
RX	MEDLINE=82046598; PubMed=6794615;	
RA	Andrews D.W., Capra J.D.;	
RT	"Amino acid sequence of the variable regions of light chains from two	
RT	idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa	
RT	group.";	
RL	Biochemistry 20:5816-5822(1981).	
CC	-I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma	
CC	globulin activity.	
CC	-----	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use as long as its content is in no way modified and this statement is not	
CC	removed.	
CC	-----	
DR	PIR; A01892; KGHUS1.	
DR	HSSP; P01625; ILVSE.	
DR	SMR; P01620; 1-109.	
DR	GO; GO:0005576; C:extracellular region; NAS.	
DR	GO; GO:0003823; F:antigen binding; NAS.	
DR	GO; GO:0006955; P:immune response; NAS.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	SMART; SM00406; IGv; 1.	
DR	PROSITE; PS50835; IG LIKE; 1.	
KW	Direct protein sequencing; Immunoglobulin domain;	
KW	Immunoglobulin V region.	
FT	DISULFID	23 89
FT	NON_TER	109 109
FT	SEQUENCE	109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
DR	Query Match	31.7%; Score 427; DB 1; Length 109;
DR	Best Local Similarity	73.1%; Pred. No. 2.8e-26;
DR	Matches	79; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
QY	144 DIETQSPGTLSPGGERATFSCRSRSHIRRRVAVYQHKPGQAPRLVIHGVNRSAGIS 203	
DB	1 EIVLTQSPGTLSPGGERATLSCRASQSVSSVSLAWYQQKPGAPRLIIYGASRRATGIP 60	
QY	204 DRFGSGSGTDFTLTIITRVEPEDPALYVCQVYGASSYTFGGTKLERK 251	

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QY 240 YTFGQGTLEK 251
Db 233 ITFGQGTLEIK 244

RESULT 2

US-60-735-988-1896
; Sequence 1896, Application US/60735988
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PP9
; CURRENT APPLICATION NUMBER: US/60/735,988
; CURRENT FILING DATE: 2005-11-14
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1896
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-735-988-1896

Query Match 70.5%; Score 949; DB 8; Length 245;
Best Local Similarity 73.8%; Pred. No. 2.1e-50;
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 2 QVQLVSGAEVKKPGASVKVSCKASGYRFSNFTVHWVRQAPGORFWMGWINPYNGNKEF 61
Db 1 QVQLVSGAEVKKPGASVKVSCKASGYRFSNFTVHWVRQAPGORFWMGWINAGNTKY 60
QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGEWGDSPQDNYMDVWGK 121
Db 61 SQKPGQRTVITRDTASTAYMELSLRSADTAVYCARVGEWGDSPQDNYMDVWGK 113
QY 122 TTIVVSSGGGGGGGGGGGGGG--LTQSPGTLSPGERATFSCRSRSHSRRAV 179
Db 114 TWVTVSSGGGGGGGGGGGGGG--LTQSPGTLSPGERATFSCRSRSHSRRAV 173
QY 180 YQHPGQAPRLVHGVSNRAGISDRFSGSGSGTDFLTITRVEPEDFALYYCOVYGAS 239
Db 174 YQKPGQPPSLLIYGASSRATGIPDRFSASGSGTDFLTITRVEPEDFALYYCOVYG-SS 232
QY 240 YTFGQGTLEK 251
Db 233 ITFGQGTLEIK 244

RESULT 3

US-60-776-665-1896
; Sequence 1896, Application US/60776665
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PP10
; CURRENT APPLICATION NUMBER: US/60/776,665
; CURRENT FILING DATE: 2006-02-27
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1896
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-776-665-1896

Query Match 70.5%; Score 949; DB 8; Length 245;
Best Local Similarity 73.8%; Pred. No. 2.1e-50;
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 2 QVQLVSGAEVKKPGASVKVSCKASGYRFSNFTVHWVRQAPGORFWMGWINPYNGNKEF 61
Db 1 QVQLVSGAEVKKPGASVKVSCKASGYRFSNFTVHWVRQAPGORFWMGWINAGNTKY 60
QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGEWGDSPQDNYMDVWGK 121

Db 61 SQKPGQRTVITRDTASTAYMELSLRSADTAVYCARVGEWGDSPQDNYMDVWGK 113
QY 122 TTIVVSSGGGGGGGGGGGGGG--LTQSPGTLSPGERATFSCRSRSHSRRAV 179
Db 114 TWVTVSSGGGGGGGGGGGGGG--LTQSPGTLSPGERATFSCRSRSHSRRAV 173
QY 180 YQHPGQAPRLVHGVSNRAGISDRFSGSGSGTDFLTITRVEPEDFALYYCOVYGAS 239
Db 174 YQKPGQPPSLLIYGASSRATGIPDRFSASGSGTDFLTITRVEPEDFALYYCOVYG-SS 232
QY 240 YTFGQGTLEK 251
Db 233 ITFGQGTLEIK 244

RESULT 4

US-11-266-444-12
; Sequence 12, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-12

Query Match 65.6%; Score 884; DB 6; Length 251;
Best Local Similarity 68.4%; Pred. No. 1.7e-46;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

QY 2 QVQLVSGAEVKKPGASVKVSCKASGYRFSNFTVHWVRQAPGORFWMGWINPYNGNKEF 61
Db 1 QVQLVSGAEVKKPGASVKVSCKASGYRFSNFTVHWVRQAPGORFWMGWINAGNTKY 60
QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGEWGDSPQDNYMDVWGK 120
Db 61 AQKPGQRTVITADTSTAYIELSLKSDTAVYCARVGEWGDSPQDNYMDVWGK 117
QY 121 GTTVIVSSGGGGGGGGGGGG--LTQSPGTLSPGERATFSCRSRSHSRRAV 178
Db 118 GTVTVSSGGGGGGGGGGGG--LTQSPGTLSPGERATFSCRSRSHSRRAV 177
QY 179 WYQHPGQAPRLVHGVSNRAGISDRFSGSGSGTDFLTITRVEPEDFALYYCOVYGAS 238
Db 178 WYQKPGQAPRLLIYGASSRATGIPDRFSASGSGTDFLTITRVEPEDFALYYCOVYG-SS 237
QY 239 SYTFGQGTLEK 251
Db 238 PRTFGQGTLEIK 250

RESULT 5

US-11-266-444-26
; Sequence 26, Application US/11266444
; GENERAL INFORMATION:


```
US-60-776-665-12
Query Match          65.6%; Score 884; DB 8; Length 251;
Best Local Similarity 68.4%; Pred. No. 1.7e-46;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

QY      2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHVHVRQAPGQRFEMMGWINPYGNKKEF 61
DB      1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHDSTKY 60

QY      62 SAKFQDRVTFTADTSANTAYMELRSADTAIVYCARVGEWGWDDSPQDNY-YMDVWGK 120
DB      61 AQKFQGRVTMTADTSTAYIELRSKSDTAVYYCARP---FYDTLTTRYVFOYFDHWGQ 117

QY      121 GTTVIVSSGGGGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSIRSRVA 178
DB      118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPTDLSLSPGERATLSCRASQSVTRGWVA 177

QY      179 WYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGAS 238
DB      178 WYQKPGQAPRLMYGASRRATGVPDFRFGSGSGTDFTLTISRLEPEDFAVYYCQVYATS 237

QY      239 SYTFGGQTKLERK 251
DB      238 PRTFGQGRLEIK 250

RESULT 9
US-60-776-665-26
; Sequence 26, Application US/60776665
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PDI
; CURRENT FILING DATE: 2006-02-27
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 26
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-776-665-26

Query Match          65.6%; Score 884; DB 8; Length 251;
Best Local Similarity 68.4%; Pred. No. 1.7e-46;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

QY      2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHVHVRQAPGQRFEMMGWINPYGNKKEF 61
DB      1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHDSTKY 60

QY      62 SAKFQDRVTFTADTSANTAYMELRSADTAIVYCARVGEWGWDDSPQDNY-YMDVWGK 120
DB      61 AQKFQGRVTMTADTSTAYIELRSKSDTAVYYCARP---FYDTLTTRYVFOYFDHWGQ 117

QY      121 GTTVIVSSGGGGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSIRSRVA 178
DB      118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPTDLSLSPGERATLSCRASQSVTRGWVA 177

QY      179 WYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGAS 238
DB      178 WYQKPGQAPRLMYGASRRATGVPDFRFGSGSGTDFTLTISRLEPEDFAVYYCQVYATS 237

QY      239 SYTFGGQTKLERK 251
DB      238 PRTFGQGRLEIK 250

RESULT 10
US-11-266-444-22
; Sequence 22, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PDI
; CURRENT FILING DATE: 2005-11-04
; NUMBER OF SEQ ID NOS: 3239
; SEQ ID NO 22
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-22

Query Match          65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 68.4%; Pred. No. 2e-46;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

QY      2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHVHVRQAPGQRFEMMGWINPYGNKKEF 61
DB      1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHDSTKY 60

QY      62 SAKFQDRVTFTADTSANTAYMELRSADTAIVYCARVGEWGWDDSPQDNY-YMDVWGK 120
DB      61 AQKFQGRVTMTADTSTAYIELRSKSDTAVYYCARP---FYDTLTTRYVFOYFDHWGQ 117

QY      121 GTTVIVSSGGGGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSIRSRVA 178
DB      118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPTDLSLSPGERATLSCRASQSVTRGWVA 177

QY      179 WYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGAS 238
DB      178 WYQKPGQAPRLMYGASRRATGVPDFRFGSGSGTDFTLTISRLEPEDFAVYYCQVYATS 237

QY      239 SYTFGGQTKLERK 251
DB      238 PRTFGQGRLEIK 250

RESULT 11
US-11-266-444-28
; Sequence 28, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PDI
; CURRENT FILING DATE: 2005-11-04
; NUMBER OF SEQ ID NOS: 3239
; SEQ ID NO 28
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-28
```


; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-28

Query Match 65.6%; Score 883; DB 6; Length 251;

Best Local Similarity 67.2%; Pred. No. 2e-46;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOAGYRFSNFTVHVVRQAPGQRFENMGWINPYNNGKEF 61

Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGEWGDSP---QDNY---Y 114

Db 61 AQKFGQRTVTADTSTSTAYIELSLKSDDTAVYICAR-----PFYDILTSYVFOY 111

Qy 115 MDVWGKGTITVIVSSGGSGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSI 172

Db 112 FDHWGQGTMTVIVSSGGSGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171

Qy 173 RSRVAVYQHKPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYC 232

Db 172 TRGWAVYQKPGQAPRLMTYGASRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYIC 231

Qy 233 QVYGASSYTFGQGTCLKERK 251

Db 232 QVYATSPRTFGQGTLEIK 250

RESULT 12

US-11-266-444-33

; Sequence 33, Application US/11266444

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat

; FILE REFERENCE: PF523P1D1

; CURRENT APPLICATION NUMBER: US/11/266,444

; CURRENT FILING DATE: 2005-11-04

; PRIOR APPLICATION NUMBER: 09/880,746

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 33

; LENGTH: 251

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-266-444-33

Query Match 65.6%; Score 883; DB 6; Length 251;

Best Local Similarity 67.2%; Pred. No. 2e-46;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOAGYRFSNFTVHVVRQAPGQRFENMGWINPYNNGKEF 61

Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGEWGDSP---QDNY---Y 114

Db 61 AQKFGQRTVTADTSTSTAYIELSLKSDDTAVYICAR-----PFYDILTSYVFOY 111

Qy 115 MDVWGKGTITVIVSSGGSGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSI 172

Db 112 FDHWGQGTMTVIVSSGGSGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171

Qy 173 RSRVAVYQHKPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYC 232

Db 172 TRGWAVYQKPGQAPRLMTYGASRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYIC 231

Qy 233 QVYGASSYTFGQGTCLKERK 251

Db 232 QVYATSPRTFGQGTLEIK 250

Db 112 FDHWGQGTMTVIVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171

Qy 173 RSRVAVYQHKPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYC 232

Db 172 TRGWAVYQKPGQAPRLMTYGASRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYIC 231

Qy 233 QVYGASSYTFGQGTCLKERK 251

Db 232 QVYATSPRTFGQGTLEIK 250

RESULT 13

US-11-266-444-43

; Sequence 43, Application US/11266444

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimula

; FILE REFERENCE: PF523P1D1

; CURRENT APPLICATION NUMBER: US/11/266,444

; CURRENT FILING DATE: 2005-11-04

; PRIOR APPLICATION NUMBER: 09/880,746

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 43

; LENGTH: 251

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-266-444-43

Query Match 65.6%; Score 883; DB 6; Length 251;

Best Local Similarity 68.4%; Pred. No. 2e-46;

Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOAGYRFSNFTVHVVRQAPGQRFENMGWINPYNNGKEF 61

Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGEWGDSPQDNY-YMDVWGK 120

Db 61 AQKFGQRTVTADTSTSTAYIELSLKSDDTAVYICAR---FYDILTYSYVFOYFDHWGQ 117

Qy 121 GTTVIVSSGGSGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSIRSRVA 178

Db 118 GTMTVIVSSGGSGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHKPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYCQVYGAS 238

Db 178 WYQKPGQAPRLMLMYGTSRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYICQYVATS 237

Qy 239 SYTFGQGTCLKERK 251

Db 238 PRTFGQGTLEIK 250

RESULT 14

US-11-266-444-127

; Sequence 127, Application US/11266444

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat

; FILE REFERENCE: PF523P1D1

; CURRENT APPLICATION NUMBER: US/11/266,444

Mon Mar 20 08:51:24 2006

121 GTTVIVSSGGGGGGGGGGSDIE--LTQSPGTLTSLSPGERATFSCRSSHSIRSRVA 178
118 GTMVTVSSGGGGGGGGGGSALETTLTQSPDTLTLSPGERATLSCRASQSVTRGWVA 177
179 WYQHKPGQAPRLVHGVSNRSGISDRFSGSGSGTDFTLTITRVEPEDEPFALYYCQVYGAS 238
178 WYQKPGQAPRLMLMYGASRRATGVPDRFSGSGSGTDFTLTISRLEPEDFAVYICQYAT 237
239 SYTFGGQTKLERK 251
238 PRTFGGQTRLEIK 250

Search completed: March 20, 2006, 07:49:46
Job time : 105 secs

Query Match 65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 68.1%; Pred. No. 2e-46;
Matches 173; Conservative 29; Mismatches 44; Indels 8; Gaps 3;
Qy 2 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHWVRQAPGQRFWMGWINPYGNKEF 61
Db 1 QVQLVQSGVEVKPGASVKVSCKASGYTFNHNHGISWVRQAPGQGLEWGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRLSADTAVYICARVGEWGWDDSPQDN--YYMDVWG 119
Db 61 AQKFGQRTVMTADTSTSTAYIELRLSKSDDTAVYICAR---PFYDTLTSVVEHYDVWG 116
Qy 120 KGTTVIVSSGGGGGGGGGGSDIE--LTQSPGTLTSLSPGERATFSCRSSHSIRSRV 177
Db 117 QGTMTVTVSSGGGGGGGGGGSALETTLTQSPDTLTLSPGERATLSCRASQSVTRGWV 176
Qy 178 WYQHKPGQAPRLVHGVSNRSGISDRFSGSGSGTDFTLTITRVEPEDEPFALYYCQVYGA 237
Db 177 AWYQKPGQAPRLMLMYGASRRATGVPDRFSGSGSGTDFTLTISRLEPEDFAVYICQYAT 236
Qy 238 SYTFGGQTKLERK 251
Db 237 PRTFGGQTRLEIK 250

RESULT 15
US-60-735-988-22
; Sequence 22, Application US/60735988
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to B Lymphocyte Stimulatc
; FILE REFERENCE: PFS23PP9
; CURRENT APPLICATION NUMBER: US/60/735,988
; CURRENT FILING DATE: 2005-11-14
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 22
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-735-988-22

Query Match 65.6%; Score 883; DB 8; Length 251;
Best Local Similarity 68.4%; Pred. No. 2e-46;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;
Qy 2 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHWVRQAPGQRFWMGWINPYGNKEF 61
Db 1 QVQLVQSGVEVKPGASVKVSCKASGYTFNHNHGISWVRQAPGQGLEWGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRLSADTAVYICARVGEWGWDDSPQDN--YYMDVWGK 120
Db 61 AQKFGQRTVMTADTSTSTAYIELRLSKSDDTAVYICAR---FYDTLTSVVEHYDVWGQ 117

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:46:30 ; Search time 16 Seconds
(without alignments)
1509.400 Million cell updates/sec

Title: US-09-673-707-1
Perfect score: 1347
Sequence: 1 MQVLEQSGAEVYKPGASVK.....QVYGASSYTFGGTKLERK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	718	53.3	249	2 S41374	single chain Fv an
2	688.5	51.1	268	2 A56446	Ig heavy chain V r
3	656	48.7	233	2 J53322	p53 specific singl
4	466	34.6	129	2 S36260	Ig heavy chain V r
5	456	33.9	129	2 S46393	Ig heavy chain V r
6	448	33.3	109	2 H30601	Ig kappa chain V-I
7	445	33.0	109	2 G30601	Ig kappa chain V-I
8	444	33.0	109	2 F30601	Ig kappa chain V-I
9	443	32.9	108	2 C30608	Ig kappa chain V-I
10	441.5	32.8	124	2 S19665	Ig heavy chain V r
11	441	32.7	107	2 PH0965	Ig kappa chain V r
12	439	32.6	124	2 S20633	Ig kappa chain - h
13	438.5	32.6	114	2 S46375	Ig kappa chain V-I
14	437	32.4	109	2 S30601	Ig kappa chain V-I
15	437	32.4	123	2 D33548	Ig heavy chain V-I
16	437	32.4	129	2 S49532	anti-Sm antibody V
17	436	32.4	109	2 G30607	Ig kappa chain V-I
18	436	32.4	109	2 D30601	Ig kappa chain V-I
19	435	32.3	129	1 K3HUNA	Ig kappa chain pre
20	435	32.3	129	2 S46369	Ig light chain var
21	435	32.3	134	2 S38643	Ig kappa chain V r
22	434	32.2	109	2 C30601	Ig kappa chain V-I
23	434	32.2	129	1 K3HUIH	Ig kappa chain pre
24	434	32.2	130	2 S20637	Ig kappa chain V r
25	433	32.1	109	2 A30608	Ig kappa chain V-I
26	433	32.1	129	2 A32274	Ig kappa chain pre
27	433	32.1	144	2 B30502	Ig heavy chain V r
28	432	32.1	109	2 F44151	Ig kappa chain V r
29	432	32.1	148	2 S29257	Ig heavy chain V r

30 431.5 32.0 118 2 S36265 Ig heavy chain V r
31 430.5 32.0 118 2 PH1666 Ig heavy chain V r
32 430 31.9 109 2 PH0963 Ig kappa chain V r
33 430 31.9 109 2 F30607 Ig kappa chain V-I
34 429 31.8 109 2 S47181 Ig kappa chain - h
35 427 31.7 109 1 K3HUIH Ig kappa chain V-I
36 426 31.6 109 1 K3HUIH Ig kappa chain V-I
37 426 31.6 128 2 S20636 Ig kappa chain V r
38 425 31.6 127 2 PH0955 Ig heavy chain V r
39 424.5 31.5 114 2 PH1667 Ig heavy chain V r
40 424 31.5 109 1 K3HUIH Ig kappa chain V-I
41 424 31.5 627 2 S14683 Ig mu chain precu
42 423.5 31.4 108 2 H44151 Ig kappa chain V r
43 423.5 31.4 136 2 S31600 Ig heavy chain V r
44 422.5 31.4 131 2 S40346 Ig kappa chain V-J
45 422 31.3 108 1 K3HUB6 Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti
A:Reference number: S41374
A:Accession: S41374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 53.3%; Score 718; DB 2; Length 249;
Best Local Similarity 55.5%; Pred. No. 4.6e-47;
Matches 142; Conservative 38; Mismatches 60; Indels 16; Gaps 3;

Qy 2 QVLEQSGAEVYKPGASVKVSCQASGYRFSNFTVHVRVQAFQRFEMGWINPYNGNKEF 61
Db 1 QVLEQSGAEVYKPGASVKVSCQASGYRFSNFTVHVRVQAFQRFEMGWINPYNGNKEF 60
Qy 62 SAKQDRVTFTADTSANTAYMELSLRSADTAVYICARVGEWDDSDPDNYV--MDVWG 119
Db 61 VPRFQDKATITADTSSNTAYLLSLTSEDVAVYICAR-----RDTLYTSLGYWG 110
Qy 120 KGTTVIVSSGGSGGG 175
Db 111 QGSTVTVSSRRGG 170
Qy 176 RVAYQHKPGQAPRLVHGVNSRASGISDRFSGSGGTDFTLTITRVRPEPFPALYQCQVY 235
Db 171 YLFWFLQPGQSPQLLYRKNLASGVDPDRFSGSGGTSFTLIRSRVEAEDGVGYTCMQH 230
Qy 236 GASSYTFGGTKLERK 251
Db 231 REYPLTFGAGTKLELK 246

RESULT 2

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/c)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally iden
A:Reference number: A56446; MUID:95229583; PMID:7713873
A:Accession: A56446

C:Accession: F30601
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human Igm autoant
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: F30601
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>
A:Cross-references: UNIPARC:UPI0000176AE3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 33.0%; Score 444; DB 2; Length 109;
Best Local Similarity 76.9%; Pred. No. 8.1e-27;
Matches 83; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 144 DIELTQSPGTLISLSPGERATFSCRSSHSIRRRVAVYQHKPGQAPRLVIHGVSNRAGIS 203
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSRYLAWYQKPGQAPRLVIYGASSRATGIP 60
Qy 204 DRFGSGSGTDFLTITRVPEDPALYCVQYGASSYTFGGTKLERK 251
Db 61 DRFTGSGSGTDFLTITRVPEDPALYCVQYGASSYTFGGTKLERK 108

RESULT 9
C30608
Ig kappa chain V-III region (Pie) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C:Accession: C30608
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human Igm autoant
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: C30608
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-108 <GON>
A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 443; DB 2; Length 108;
Best Local Similarity 76.9%; Pred. No. 9.5e-27;
Matches 83; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 144 DIELTQSPGTLISLSPGERATFSCRSSHSIRRRVAVYQHKPGQAPRLVIHGVSNRAGIS 203
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSRYLAWYQKPGQAPRLVIYGASSRATGIP 60
Qy 204 DRFGSGSGTDFLTITRVPEDPALYCVQYGASSYTFGGTKLERK 251
Db 61 DRFGSGSGTDFLTITRVPEDPALYCVQYGASSYTFGGTKLERK 108

RESULT 10
S19665
Ig heavy chain V region (alpha-phOx15) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C:Accession: S19665; S24442
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19665
A:Molecule type: mRNA
A:Residues: 1-124 <WAR>
A:Cross-references: UNIPARC:UPI0000176B80; EMBL:X61647

R.; Jones, P.T.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24442
A:Accession: S24442
A:Molecule type: mRNA
A:Residues: 1-40; GUSGWDGSLTWTQSIDLK', 61-118, 'T', 120-124 <JON>
A:Cross-references: UNIPARC:UPI000115F86; EMBL:X61647; NID:G37667; PIDN:CAA43828.1; PID
A>Note: the difference for residues 41-60 results from misplacement of 10 bases in the s
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 32.8%; Score 441.5; DB 2; Length 124;
Best Local Similarity 65.6%; Pred. No. 1.4e-26;
Matches 86; Conservative 14; Mismatches 20; Indels 11; Gaps 2;

QY 2 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLRWGMMGWSAYNGTKY 61
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLRWGMMGWSAYNGTKY 60

QY 62 SAKFQDRVFTADTSANTAYMELRSLSRSDTAIVYCARVGEWGDSDPOD---NYVMV 117
DB 61 AQKLQGRVNTTSTSTAYMELRSLSRSDTAIVYCVRL-----LPKRTATLHYIDV 113

QY 118 WKGKTTIVSS 128
DB 114 WKGKTLTVSS 124

RESULT 11
IG kappa chain V region (G6+ CLL-BRA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: PH0965
R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0965
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-107 <MAR>
A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI000176A2B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-21/Region: framework 1
F:14-89/Domain: immunoglobulin homology <IMM>
F:22-32/Region: complementarity-determining 1
F:33-48/Region: framework 2
F:49-54/Region: complementarity-determining 2
F:55-87/Region: framework 3
F:88-95/Region: complementarity-determining 3

Query Match 32.7%; Score 441; DB 2; Length 107;
Best Local Similarity 78.1%; Pred. No. 1.3e-26;
Matches 82; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 147 LTQSPGTLSPGGERATFSCRSISRVRVAVYQHKGQAPRLVIHGVSNRAGISDRP 206
DB 2 LTQSPGTLSPGGERATLSCRASQSVSSYLAIVYQKPGQAPRLIIYGTSSRATGIPDRF 61

QY 207 SGSGSGTDFTLTITRVEPEDFALYICQVYGASSYTFGGTKLERK 251
DB 62 SGSGSGTDFTLTISRLEPEDFAVYICQYGSRRYTFGGTKVEIK 106

RESULT 12
S20633
IG kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C:Accession: S20633

R.; Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20633
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-124 <LEE>
A:Cross-references: UNIPARC:UPI00001163D9; EMBL:Z11891; NID:G33185; PIDN:CAA77945.1; PI
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-107/Domain: immunoglobulin homology <IMM>

Query Match 32.6%; Score 439; DB 2; Length 124;
Best Local Similarity 77.4%; Pred. No. 2.2e-26;
Matches 82; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 144 DIETQSPGTLSPGGERATFSCRSISRVRVAVYQHKGQAPRLVIHGVSNRAGIS 203
DB 17 EIVLTQSPGTLSPGGERATLSCRASQSVSYLAIVYQKPGQAPRLIIYGTSSRATGIP 76

QY 204 DRFSGSGSGTDFTLTITRVEPEDFALYICQVYGASSYTFGGTKLE 249
DB 77 DRVSGSGSGTDFTLTISRLEPEDFAVYICQYGSSTYTFGGTKLE 122

RESULT 13
S46375
IG kappa chain V-J region (T33-5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46375; S38648
R; Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46375
A:Molecule type: mRNA
A:Residues: 1-114 <BEN>
A:Cross-references: UNIPARC:UPI0001165A8; EMBL:Z27176; NID:G415967; PIDN:CAA81700.1; P
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:20-95/Domain: immunoglobulin homology <IMM>

Query Match 32.6%; Score 438.5; DB 2; Length 114;
Best Local Similarity 78.0%; Pred. No. 2.2e-26;
Matches 85; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 144 DIETQSPGTLSPGGERATFSCRSISRVRVAVYQHKGQAPRLVIHGVSNRAGIS 203
DB 5 EIVLTQSPGTLSPGGERATLSCRASQSVSSYLAIVYQKPGQAPRLIIYGTSSRATGIP 64

QY 204 DRFSGSGSGTDFTLTITRVEPEDFALYICQVYGAS-SYTFGGTKLERK 251
DB 65 DRFSGSGSGTDFTLTISRLEPEDFAVYICQYGSPPYTFGGTKLEIK 113

RESULT 14
B30601
IG kappa chain V-III region (Glo) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C:Accession: B30601
R; Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoan
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: B30601
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>
A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Search completed: March 20, 2006, 07:48:06
Job time : 17 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:47:50 ; Search time 216 Seconds
(without alignments)
1605.883 Million cell updates/sec

Title: US-09-673-707-1

Perfect score: 1347

Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYGASSYTFQGFKLERK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues
Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US066_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US073_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US074_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US075_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US076_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US077_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US078_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US079_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1347	100.0	251	26	US-09-673-707-1	Sequence 1, Appl
2	949	70.5	245	1	PCT-US01-19110-1896	Sequence 1896, Ap
3	949	70.5	245	1	PCT-US02-36496-1896	Sequence 1896, Ap
4	949	70.5	245	28	US-09-880-748-1896	Sequence 1896, Ap
5	949	70.5	245	32	US-10-293-418-1896	Sequence 1896, Ap
6	949	70.5	245	40	US-11-054-515-1896	Sequence 1896, Ap
7	949	70.5	245	51	US-60-725-626-1896	Sequence 1896, Ap
8	927.5	68.9	281	35	US-10-535-764-1896	Sequence 186, Ap
9	910	67.6	247	1	PCT-US02-40597-56	Sequence 56, Appl
10	910	67.6	247	1	PCT-US04-13900-56	Sequence 56, Appl
11	910	67.6	247	33	US-10-322-673-56	Sequence 56, Appl
12	910	67.6	247	39	US-10-981-465-56	Sequence 56, Appl
13	910	67.6	247	39	US-10-981-621-56	Sequence 56, Appl
14	910	67.6	247	39	US-10-981-673-56	Sequence 56, Appl
15	910	67.6	247	39	US-10-981-691-56	Sequence 56, Appl
16	896.5	66.6	263	34	US-10-422-628-14	Sequence 14, Appl
17	884	65.6	251	1	PCT-US01-19110-12	Sequence 12, Appl
18	884	65.6	251	1	PCT-US01-19110-26	Sequence 26, Appl
19	884	65.6	251	1	PCT-US02-36496-12	Sequence 12, Appl
20	884	65.6	251	1	PCT-US02-36496-26	Sequence 26, Appl
21	884	65.6	251	28	US-09-880-748-12	Sequence 12, Appl
22	884	65.6	251	28	US-09-880-748-26	Sequence 26, Appl
23	884	65.6	251	32	US-10-293-418-12	Sequence 12, Appl
24	884	65.6	251	32	US-10-293-418-26	Sequence 26, Appl
25	884	65.6	251	40	US-11-054-515-12	Sequence 12, Appl
26	884	65.6	251	40	US-11-054-515-26	Sequence 26, Appl
27	884	65.6	251	51	US-60-725-626-12	Sequence 12, Appl
28	884	65.6	251	51	US-60-725-626-26	Sequence 26, Appl
29	883	65.6	251	1	PCT-US01-19110-22	Sequence 22, Appl
30	883	65.6	251	1	PCT-US01-19110-28	Sequence 28, Appl
31	883	65.6	251	1	PCT-US01-19110-33	Sequence 33, Appl
32	883	65.6	251	1	PCT-US01-19110-43	Sequence 43, Appl
33	883	65.6	251	1	PCT-US01-19110-127	Sequence 127, Appl
34	883	65.6	251	1	PCT-US02-36496-22	Sequence 22, Appl
35	883	65.6	251	1	PCT-US02-36496-28	Sequence 28, Appl
36	883	65.6	251	1	PCT-US02-36496-33	Sequence 33, Appl
37	883	65.6	251	1	PCT-US02-36496-43	Sequence 43, Appl
38	883	65.6	251	1	PCT-US02-36496-127	Sequence 127, Appl
39	883	65.6	251	28	US-09-880-748-22	Sequence 22, Appl
40	883	65.6	251	28	US-09-880-748-28	Sequence 28, Appl
41	883	65.6	251	28	US-09-880-748-33	Sequence 33, Appl
42	883	65.6	251	28	US-09-880-748-43	Sequence 43, Appl
43	883	65.6	251	28	US-09-880-748-127	Sequence 127, Appl
44	883	65.6	251	32	US-10-293-418-22	Sequence 22, Appl
45	883	65.6	251	32	US-10-293-418-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-673-707-1
; Sequence 1, Application US/09673707
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.

```
; APPLICANT: Bera, Tapan K.
; APPLICANT: Kennedy, Paul E.
; APPLICANT: Berger, Edward A.
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Immunotoxin Directed Against the HIV-1
; TITLE OF INVENTION: gp120 Envelope Glycoprotein
; FILE REFERENCE: 015280-356100US
; CURRENT APPLICATION NUMBER: US/09/673,707
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: WO PCT/US99/12909
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: US 60/088,860
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:3B3(Fv) amino
; OTHER INFORMATION: acid sequence
US-09-673-707-1

Query Match      100.0%; Score 1347; DB 26; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.2e-107;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWRQAPGQRFEMWGWINPYNGNKE 60
Db 1 MQVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWRQAPGQRFEMWGWINPYNGNKE 60

Qy 61 FSAKFDQRTVTADTSANTAYMELSLRSADTAVYVCARVGEWGDSPQDNYMDVWGK 120
Db 61 FSAKFDQRTVTADTSANTAYMELSLRSADTAVYVCARVGEWGDSPQDNYMDVWGK 120

Qy 121 GTTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSSHSIRSRVAV 180
Db 121 GTTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSSHSIRSRVAV 180

Qy 181 QHKPQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGASSY 240
Db 181 QHKPQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGASSY 240

Qy 241 TFGQGTCLERK 251
Db 241 TFGQGTCLERK 251

RESULT 2
PCT-US01-19110-1896
; Sequence 1896, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0

Query Match      70.5%; Score 949; DB 1; Length 245;
Best Local Similarity 73.8%; Pred. No. 1.3e-72;
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWRQAPGQRFEMWGWINPYNGNKEF 61
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLLEMMGWINAGNNTKY 60

Qy 62 SAKFDQRTVTADTSANTAYMELSLRSADTAVYVCARVGEWGDSPQDNYMDVWGK 121
Db 61 SAKFDQRTVTADTSANTAYMELSLRSADTAVYVCAREG-----PGYYGMDVWGQG 113

Qy 122 TTVIVSSGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSSHSIRSRVAV 179
Db 114 TMVTIVSSGGGGGGGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

Qy 180 YQHKPQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGASS 239
Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSGTDFTLTISRLEPEDFAVYVCQYQYG-SS 232

Qy 240 YTFGQGTCLERK 251
Db 233 ITFGQGTCLERK 244

RESULT 3
PCT-US02-36496-1896
; Sequence 1896, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1896
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1896

Query Match      70.5%; Score 949; DB 1; Length 245;
Best Local Similarity 73.8%; Pred. No. 1.3e-72;
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWRQAPGQRFEMWGWINPYNGNKEF 61
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLLEMMGWINAGNNTKY 60

Qy 62 SAKFDQRTVTADTSANTAYMELSLRSADTAVYVCARVGEWGDSPQDNYMDVWGK 121
Db 61 SAKFDQRTVTADTSANTAYMELSLRSADTAVYVCAREG-----PGYYGMDVWGQG 113

Qy 122 TTVIVSSGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSSHSIRSRVAV 179
Db 114 TMVTIVSSGGGGGGGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

Qy 180 YQHKPQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGASS 239
Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSGTDFTLTISRLEPEDFAVYVCQYQYG-SS 232

Qy 240 YTFGQGTCLERK 251
Db 233 ITFGQGTCLERK 244
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Db 233 ITFGQGTREIK 244

RESULT 4

US-09-880-748-1896

Sequence 1896, Application US/09880748

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1896

LENGTH: 245

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1896

Query Match 70.5%; Score 949; DB 28; Length 245;

Best Local Similarity 73.8%; Pred. No. 1.3e-72;

Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWYRQAPGQRFPMWCHINPYNGNKEF 61

Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWYRQAPGQRFPMWCHINAGNTKY 60

Qy 62 SAKFDQRTVTTADTSANTAYMELRSLSRSDTAVYCARVGEWGWDDSPQDNYMDVWGK 121

Db 61 SQRFQGRVTITRDTASATAYMELSLRSEDATVYICAREG-----PGYYGMDVWGQ 113

Qy 122 TTVIVSGGGSGGGSGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179

Db 114 TMTVSSGGSGGGSGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

Qy 180 YQHPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYICQVYGASS 239

Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSGTDFTLTISRLEPEDFAVYICQYQY-G-SS 232

Qy 240 YTFGQGTLEIK 251

Db 233 ITFGQGTREIK 244

RESULT 5

US-10-293-418-1896

Sequence 1896, Application US/10293418

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWYRQAPGQRFPMWCHINPYNGNKEF 61

Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWYRQAPGQRFPMWCHINAGNTKY 60

Qy 62 SAKFDQRTVTTADTSANTAYMELRSLSRSDTAVYCARVGEWGWDDSPQDNYMDVWGK 121

Db 61 SQRFQGRVTITRDTASATAYMELSLRSEDATVYICAREG-----PGYYGMDVWGQ 113

Qy 122 TTVIVSGGGSGGGSGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179

Db 114 TMTVSSGGSGGGSGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

Qy 180 YQHPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYICQVYGASS 239

Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSGTDFTLTISRLEPEDFAVYICQYQY-G-SS 232

Qy 240 YTFGQGTLEIK 251

Db 233 ITFGQGTREIK 244

RESULT 6

US-11-054-515-1896

Sequence 1896, Application US/11054515

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1896

LENGTH: 245

TYPE: PRT

Query Match	70.5%; Score 949; DB 40; Length 245;	Best Local Similarity 73.8%; Pred. No. 1.3e-72;	Mismatches 21; Mismatches 35; Indels 10; Gaps 3;
Qy	2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGWINPYNGNKEF 61		
Db	1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLLEWGMWVINGNNTKY 60		
Qy	62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGEWGWDDSPQDNYMDVWVGK 121		
Db	61 SQKFGQRTVITRTDTSASTAYMELSLRSADTAVYYCARVGEWGWDDSPQDNYMDVWVGQ 113		
Qy	122 TTIVVSGGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179		
Db	114 TMTVSSGGGGGGGGGGGGGSALETTLTQSPGTLSLSPGERATLSCRAQAIGSNYLAW 173		
Qy	180 YQHKPGQAPRLVIHGVSNRASGISDRFSGSGSDTFTLTITRVEPEDFALYYCQVYGASS 239		
Db	174 YQKFGQPPSLIYGASSRATGIPDRFSAGSGDTFTLTISRLEPEDFAVYYCQYQV-G-SS 232		
Qy	240 YTFGGQTKLERK 251		
Db	233 ITFGQGTRLERK 244		
RESULT 7			
US-60-725-626-1896			
; Sequence 1896, Application US/60725626			
; GENERAL INFORMATION:			
; APPLICANT: Ruben et al.			
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato			
; FILE REFERENCE: PF523PP8			
; CURRENT APPLICATION NUMBER: US/60/725,626			
; CURRENT FILING DATE: 2005-10-13			
; NUMBER OF SEQ ID NOS: 3247			
; SEQ ID NO 1896			
; LENGTH: 245			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-60-725-626-1896			
Query Match	70.5%; Score 949; DB 51; Length 245;	Best Local Similarity 73.8%; Pred. No. 1.3e-72;	Mismatches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;
Qy	2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGWINPYNGNKEF 61		
Db	1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLLEWGMWVINGNNTKY 60		
Qy	62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGEWGWDDSPQDNYMDVWVGK 121		
Db	61 SQKFGQRTVITRTDTSASTAYMELSLRSADTAVYYCARVGEWGWDDSPQDNYMDVWVGQ 113		
Qy	122 TTIVVSGGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179		
Db	114 TMTVSSGGGGGGGGGGGGGSALETTLTQSPGTLSLSPGERATLSCRAQAIGSNYLAW 173		
Qy	180 YQHKPGQAPRLVIHGVSNRASGISDRFSGSGSDTFTLTITRVEPEDFALYYCQVYGASS 239		
Db	174 YQKFGQPPSLIYGASSRATGIPDRFSAGSGDTFTLTISRLEPEDFAVYYCQYQV-G-SS 232		
Qy	240 YTFGGQTKLERK 251		
Db	233 ITFGQGTRLERK 244		
RESULT 8			
US-10-535-764-186			
; Sequence 186, Application US/10535764			
; GENERAL INFORMATION:			
; APPLICANT: Human Genome Sciences, Inc.			
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL			
; FILE REFERENCE: PF585PCT			
; CURRENT APPLICATION NUMBER: PCT/US02/40597			
; CURRENT FILING DATE: 2002-12-18			
; PRIOR APPLICATION NUMBER: 60/341,237			
; PRIOR FILING DATE: 2001-12-20			
; PRIOR APPLICATION NUMBER: 60/369,877			
; PRIOR FILING DATE: 2002-04-05			
; PRIOR APPLICATION NUMBER: 60/384,828			
; PRIOR FILING DATE: 2002-06-04			
; PRIOR APPLICATION NUMBER: 60/396,591			
; PRIOR FILING DATE: 2002-07-18			
; PRIOR APPLICATION NUMBER: 60/403,370			
; PRIOR FILING DATE: 2002-08-15			
; PRIOR APPLICATION NUMBER: 60/425,737			
; PRIOR FILING DATE: 2002-11-13			
; NUMBER OF SEQ ID NOS: 72			
; SEQ ID NO 56			
; LENGTH: 247			
; TYPE: PRT			


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; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
; US-10-981-621-56

Query Match          67.6%; Score 910; DB 39; Length 247;
Best Local Similarity 69.4%; Pred. No. 2.8e-69;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy 2 QVQLSGAEVKKPGASVKVSQASGYRFSNFTVHVWVQAPGQRFVWGMWNPVGNKEF 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVQSGAEVKKPGASVKVSQASGYTFSTYGITVWVQAPGQGLEWMGWISAYNGK 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 SAKFDQRTVFTADTSANTAYMELSLRSADTAVVYCARVGEWGWDDSPQDNY---YMDV 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VQLQGRVTWTTDTSTVTVMELTSLRSDTAVVYCARRG-----NNYRFGYDFW 111
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 119 GKTTIVSSGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRHSIRSR 176
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 GQGLTVTVSSGGGGGGGGGGGGSALETTLTQSPGTLSPGERATLSCRASQSISS 171
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 177 VAWYQHKGQAPRLVHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCVYG 236
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 LAWYQQKPGAPRLIYGASSRAIGIPDRFSGSGSGTDFTLTISRLEAEDFVAVYCO 231
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 237 ASSVTFGGQTKLERK 251
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 SSPITFGQTRLEIK 246
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-981-621-56
; Sequence 56, Application US/10981621
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D1
; CURRENT APPLICATION NUMBER: US/10/981,621
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15

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; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
; US-10-981-621-56

Query Match          67.6%; Score 910; DB 39; Length 247;
Best Local Similarity 69.4%; Pred. No. 2.8e-69;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy 2 QVQLSGAEVKKPGASVKVSQASGYRFSNFTVHVWVQAPGQRFVWGMWNPVGNKEF 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVQSGAEVKKPGASVKVSQASGYTFSTYGITVWVQAPGQGLEWMGWISAYNGK 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 SAKFDQRTVFTADTSANTAYMELSLRSADTAVVYCARVGEWGWDDSPQDNY---YMDV 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VQLQGRVTWTTDTSTVTVMELTSLRSDTAVVYCARRG-----NNYRFGYDFW 111
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 119 GKTTIVSSGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRHSIRSR 176
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 GQGLTVTVSSGGGGGGGGGGGGSALETTLTQSPGTLSPGERATLSCRASQSISS 171
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 177 VAWYQHKGQAPRLVHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCVYG 236
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 LAWYQQKPGAPRLIYGASSRAIGIPDRFSGSGSGTDFTLTISRLEAEDFVAVYCO 231
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 237 ASSVTFGGQTKLERK 251
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 SSPITFGQTRLEIK 246
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-10-981-673-56
; Sequence 56, Application US/10981673
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D2
; CURRENT APPLICATION NUMBER: US/10/981,673
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15

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Db 61 SQKFGQGRVTITRDTASTAYMELSLRSEDVAVYVCAREG-----PGYYGMDVWGQG 113
QY 122 TTIVVSSGGGGGGGGGGGGSDIE--LTQSPGTLTSLSPGERATFSCRSSSHRSRRVAW 179
Db 114 TMTVSSGGGGGGGGGGGGSALETTLTQSPGTLTSLSPGERATLSCRASQAIGSNYLAW 173
QY 180 YQHKPGQAPRLVTHGVNSRASGTSDFRSGSGGTDTFTLTITRVEPEDFALYYCQVYGASS 239
Db 174 YQKPGQAPRLVTHGVNSRASGTSDFRSGSGGTDTFTLTITRVEPEDFALYYCQVYG-SS 232
QY 240 YTFGQGTCLERK 251
Db 233 ITFGQGTCLERK 250

RESULT 2
US-11-054-515-12
; Sequence 12, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-12

Query Match 65.6%; Score 884; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 1.9e-54;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;
QY 2 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHDDSTKY 60
QY 62 SAKFQDRVTFTADTSTANTAYMELSLRSADTAVYVCARVSGWDDSPQDNY-YMDVWGK 120
Db 61 AQKFGQGRVTMTADTSTSTAYIELSLKSDDTAVYVCARP---FYDTLTRYVVFQFDHWGQ 117
QY 121 GTTVIVSSGGGGGGGGGGGGSDIE--LTQSPGTLTSLSPGERATFSCRSSSHRSRRVA 178
Db 118 GTMTVSSGGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177
QY 179 WYQHKPGQAPRLVTHGVNSRASGTSDFRSGSGGTDTFTLTITRVEPEDFALYYCQVYGAS 238
Db 178 WYQKPGQAPRLVTHGVNSRASGTSDFRSGSGGTDTFTLTITRVEPEDFALYYCQVYATS 237

QY 239 SYTFGQGTCLERK 251
Db 238 PRTEGQGTCLERK 250
RESULT 3
US-11-054-515-26
; Sequence 26, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 26
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-26

Query Match 65.6%; Score 884; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 1.9e-54;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;
QY 2 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKPGASVKVSCKASGYTFSNHHGISWVRQAPGQGLEWVGWISGHDDSTKY 60
QY 62 SAKFQDRVTFTADTSTANTAYMELSLRSADTAVYVCARVSGWDDSPQDNY-YMDVWGK 120
Db 61 AQKFGQGRVTMTADTSTSTAYIELSLKSDDTAVYVCARP---FYDTLTRYVVFQFDHWGQ 117
QY 121 GTTVIVSSGGGGGGGGGGGGSDIE--LTQSPGTLTSLSPGERATFSCRSSSHRSRRVA 178
Db 118 GTMTVSSGGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177
QY 179 WYQHKPGQAPRLVTHGVNSRASGTSDFRSGSGGTDTFTLTITRVEPEDFALYYCQVYGAS 238
Db 178 WYQKPGQAPRLVTHGVNSRASGTSDFRSGSGGTDTFTLTITRVEPEDFALYYCQVYATS 237
QY 239 SYTFGQGTCLERK 251
Db 238 PRTEGQGTCLERK 250
RESULT 4
US-11-054-515-22
; Sequence 22, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:

```
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 22
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-22

Query Match 65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 2.2e-54;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVQLQSGAEVKKPGASVKVSQCOASGYRFSNFTVHWVRQAPGQRFWMGWINPYNNGKEF 61
Db 1 QVQLVQSGVEVKPGASVKVSCKASGYTFSNHGISWVRQAPGQGLEWVGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYICARVGEWGWDDSPQNY-Y 114
Db 61 AQKFGQGRVTMTADTSTSTAVIELRSLSKSDDTAVYICAR-----PFYDILTSYVFOY 111
Qy 115 MDVWGKGTIVIVSSGGSGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHI 172
Db 112 FDHWGQGTMTVTVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRAQSV 171
Qy 173 RSRRAVYQHKPGAPRLVIHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYVC 232
Db 172 TRGVWVYQKPGAPRLMYGASRRATGVDPDRFSGSGGTDFTLTISRLPEDFAVYVC 231
Qy 233 SYTFGQGTQKLERK 251
Db 232 PRTEGQGTTRLEIK 250

RESULT 5
US-11-054-515-28
; Sequence 28, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 10/293,418
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 28
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-28

Query Match 65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 67.2%; Pred. No. 2.2e-54;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

Qy 2 QVQLQSGAEVKKPGASVKVSQCOASGYRFSNFTVHWVRQAPGQRFWMGWINPYNNGKEF 61
Db 1 QVQLVQSGVEVKPGASVKVSCKASGYTFSNHGISWVRQAPGQGLEWVGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYICARVGEWGWDDSP---QDNY---Y 114
Db 61 AQKFGQGRVTMTADTSTSTAVIELRSLSKSDDTAVYICAR-----PFYDILTSYVFOY 111
Qy 115 MDVWGKGTIVIVSSGGSGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHI 172
Db 112 FDHWGQGTMTVTVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRAQSV 171
Qy 173 RSRRAVYQHKPGAPRLVIHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYVC 232
Db 172 TRGVWVYQKPGAPRLMYGASRRATGVDPDRFSGSGGTDFTLTISRLPEDFAVYVC 231
Qy 233 QVYGASSYTFGQGTQKLERK 251
Db 232 QYATSPRTFGQGTTRLEIK 250

RESULT 6
US-11-054-515-33
; Sequence 33, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 33
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-53

Query Match      65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 67.8%; Pred. No. 2.2e-54;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVWVQAPGQRFEMWGWINPYNGNKEF 61
DB 1 QVQLVQSGVEVKKPGASVKVCKASGYTFNTHGHSWVRQAPGQGLEWVGWISGHDSTKY 60
QY 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAVYICARVGEWGWDDSP-----QDNY---Y 114
DB 61 AOKFQGRVTMTADTSTSTAYIELRSLKSDDTAVYICAR-----PFYDILTYSYVQY 111
QY 115 MDVWVGKTTIVSSGGSGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSSHSI 172
DB 112 FDHWGQGTVMVTVSSGGSGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171
QY 173 RSRRAVWYQHPGQAPRLVHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYC 232
DB 172 TRGVAVYQKPGQAPRLLMYGTSSRATGVPDRFSGSGSGTDFTLTISRLEPEDFAVYVC 231
QY 233 QVYGASSYTFGGTKLERK 251
DB 232 QVATSPRTFGQTRLEIK 250
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RESULT 7
US-11-054-515-43
; Sequence 43, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 43
; LENGTH: 251
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-11-054-515-43

Query Match      65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 2.2e-54;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVWVQAPGQRFEMWGWINPYNGNKEF 61
DB 1 QVQLVQSGVEVKKPGASVKVCKASGYTFNTHGHSWVRQAPGQGLEWVGWISGHDSTKY 60
QY 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAVYICARVGEWGWDDSPDNY--YMDVWVGK 120
DB 61 AOKFQGRVTMTADTSTSTAYIELRSLKSDDTAVYICARP---FYDTLTSYVQYFDHWGQ 117
QY 121 GTTVIVSSGGSGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSSHSIRRRVA 178
DB 118 GTWVTVSSGGSGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177
QY 179 WYQHPGQAPRLVHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCYGVYV 238
DB 178 WYQHPGQAPRLLMYGTSSRATGVPDRFSGSGSGTDFTLTISRLEPEDFAVYVCQYV 237
QY 239 SYTFGGQTKLERK 251
DB 238 PRTEGQGTTRLEIK 250
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```
RESULT 8
US-11-054-515-127
; Sequence 127, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 127
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-127
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Query Match      65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 68.1%; Pred. No. 2.2e-54;
Matches 173; Conservative 29; Mismatches 44; Indels 8; Gaps 3;

QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVWVQAPGQRFEMWGWINPYNGNKEF 61
DB 1 QVQLVQSGVEVKKPGASVKVCKASGYTFNTHGHSWVRQAPGQGLEWVGWISGHDSTKY 60
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Mon Mar 20 08:51:24 2006

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; Sequence 216, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 216
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-216

Query Match 65.5%; Score 882; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 2.6e-54;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGVRFSNFTVHWVRQAPGQGFVWMGWINPYNKNEF 61
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNHSWVRQAPGQGLEWVGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRSADTAIVYCARVGEWGDSPQDNY-YMDVWGK 120
Db 61 AQKFGQRTVTADTSTSTAYIELRLSKSDDTAVVYCARP---FYDTLTSYVFQYFDHWGQ 117
Qy 121 GTTVIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSLSPGERATFSCRSHSRRA 178
Db 118 GTMTVSSGGGGSGGGSGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177
Qy 179 WYQHPGQAPRLVTHGVNRSAGISDRFSGSGGTDFTLITRVEPEDFALYYCQVYGAS 238
Db 178 WYQHPGQAPRLVTHGVNRRATGVPDRFSGSESGTDFTLITRLEPEDFAVYYCQVYATS 237
Qy 239 SYTFGGQTKLERK 251
Db 238 PRTFGGQTRLEIK 250

RESULT 12
US-11-054-515-171
; Sequence 171, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 216
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-216

Query Match 65.5%; Score 882; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 2.6e-54;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGVRFSNFTVHWVRQAPGQGFVWMGWINPYNKNEF 61
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNHSWVRQAPGQGLEWVGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRSADTAIVYCARVGEWGDSPQDNY-YMDVWGK 120
Db 61 AQKFGQRTVTADTSTSTAYIELRLSKSDDTAVVYCARP---FYDTLTSYVFQYFDHWGQ 117
Qy 121 GTTVIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSLSPGERATFSCRSHSRRA 178
Db 118 GTMTVSSGGGGSGGGSGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177
Qy 179 WYQHPGQAPRLVTHGVNRSAGISDRFSGSGGTDFTLITRVEPEDFALYYCQVYGAS 238
Db 178 WYQHPGQAPRLVTHGVNRRATGVPDRFSGSESGTDFTLITRLEPEDFAVYYCQVYATS 237
Qy 239 SYTFGGQTKLERK 251
Db 238 PRTFGGQTRLEIK 250

RESULT 13
US-11-054-515-317
; Sequence 317, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 317
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-317

Query Match      65.4%; Score 881; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 3.1e-54;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVQLEQSGAEVKKPGASVKVSQAQSGYRFNSFTVHVRQAPGQRFPEWVGWIPNGNKEF 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSSNHGISWVRQAPGQGLEWGWISGHDSTKY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYYCARVGEWGDSPQDNY-YMDVWGK 120
    : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AQKFGQGRVTMTADTSTSTAYIELSLKSDDTAVYYCARP---FYDTLTTRYVQYFDHWGQ 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 GTTVIVSSGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 GTWVTVSSGGGGGGGGGGGGSALETTLTQSPDTLSLPGKRAATLSCRASQSVTRGWVA 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 179 WYQHKPGQAPRLVTHGVSNRASGISDRFSGSGGTDFTLTIITRVEPDEPFAFYCCQVYCAS 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 WYQKPGQAPRLMYGSRRAATGVPDRFSGSGGTDFTLTIISRLPEPDEFAFYCCQVYCAS 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 239 SYTFGGQGTLEK 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 PRTEGQGTLEIK 250
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-11-054-515-27
; Sequence 27, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 34
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-34

Query Match      65.3%; Score 880; DB 7; Length 251;
Best Local Similarity 68.0%; Pred. No. 3.6e-54;
Matches 172; Conservative 30; Mismatches 45; Indels 6; Gaps 3;
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```
; SEQ ID NO 27
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-27

Query Match      65.3%; Score 880; DB 7; Length 251;
Best Local Similarity 68.0%; Pred. No. 3.6e-54;
Matches 172; Conservative 30; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVQLEQSGAEVKKPGASVKVSQAQSGYRFNSFTVHVRQAPGQRFPEWVGWIPNGNKEF 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSSNHGISWVRQAPGQGLEWGWISGHDSTKY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYYCARVGEWGDSPQDNY-YMDVWGK 120
    : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AQKFGQGRVTMTADTSTSTAYIELSLKSDDTAVYYCARP---FYDTLTTRYVQYFDHWGQ 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 GTTVIVSSGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 GTWVTVSSGGGGGGGGGGGGSALETTLTQSPDTLSLPGKRAATLSCRASQSVTRGWVA 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 179 WYQHKPGQAPRLVTHGVSNRASGISDRFSGSGGTDFTLTIITRVEPDEPFAFYCCQVYCAS 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 WYQKPGQAPRLMYGSRRAATGVPDRFSGSGGTDFTLTIISRLPEPDEFAFYCCQVYCAS 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 239 SYTFGGQGTLEK 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 PRTEGQGTLEIK 250
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-11-054-515-34
; Sequence 34, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 34
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-34

Query Match      65.3%; Score 880; DB 7; Length 251;
Best Local Similarity 68.0%; Pred. No. 3.6e-54;
Matches 172; Conservative 30; Mismatches 45; Indels 6; Gaps 3;
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:48:00 ; Search time 69 Seconds
(without alignments)
1519.930 Million cell updates/sec

Title: US-09-673-707-1
Perfect score: 1347
Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYQASSYTFGGQTKLERK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949	70.5	245	3	US-09-880-748-1896
2	949	70.5	245	4	US-10-293-418-1896
3	910	67.6	247	4	US-10-322-673-56
4	910	67.6	247	5	US-10-981-465-56
5	910	67.6	247	5	US-10-981-621-56
6	910	67.6	247	5	US-10-981-673-56
7	910	67.6	247	5	US-10-981-691-56
8	896.5	66.6	263	4	US-10-422-628-14
9	884	65.6	251	3	US-09-880-748-12
10	884	65.6	251	3	US-09-880-748-26
11	884	65.6	251	4	US-10-293-418-12
12	884	65.6	251	4	US-10-293-418-26
13	883	65.6	251	3	US-09-880-748-22
14	883	65.6	251	3	US-09-880-748-28
15	883	65.6	251	3	US-09-880-748-33
16	883	65.6	251	3	US-09-880-748-43
17	883	65.6	251	3	US-09-880-748-127
18	883	65.6	251	4	US-10-293-418-22
19	883	65.6	251	4	US-10-293-418-28
20	883	65.6	251	4	US-10-293-418-33
21	883	65.6	251	4	US-10-293-418-43
22	883	65.6	251	4	US-10-293-418-127
23	882	65.5	251	3	US-09-880-748-17
24	882	65.5	251	3	US-09-880-748-30
25	882	65.5	251	3	US-09-880-748-216
26	882	65.5	251	4	US-10-293-418-17
27	882	65.5	251	4	US-10-293-418-30

28	882	65.5	251	4	US-10-293-418-216	Sequence 216, App
29	881	65.4	251	3	US-09-880-748-171	Sequence 171, App
30	881	65.4	251	3	US-09-880-748-317	Sequence 317, App
31	881	65.4	251	4	US-10-293-418-171	Sequence 171, App
32	881	65.4	251	4	US-10-293-418-317	Sequence 317, App
33	880	65.3	251	3	US-09-880-748-27	Sequence 27, Appl
34	880	65.3	251	3	US-09-880-748-34	Sequence 34, Appl
35	880	65.3	251	3	US-09-880-748-102	Sequence 102, App
36	880	65.3	251	3	US-09-880-748-238	Sequence 238, App
37	880	65.3	251	3	US-09-880-748-295	Sequence 295, App
38	880	65.3	251	4	US-10-293-418-27	Sequence 27, Appl
39	880	65.3	251	4	US-10-293-418-34	Sequence 34, Appl
40	880	65.3	251	4	US-10-293-418-102	Sequence 102, App
41	880	65.3	251	4	US-10-293-418-238	Sequence 238, App
42	880	65.3	251	4	US-10-293-418-295	Sequence 295, App
43	879	65.3	251	3	US-09-880-748-23	Sequence 23, Appl
44	879	65.3	251	3	US-09-880-748-29	Sequence 29, Appl
45	879	65.3	251	3	US-09-880-748-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-880-748-1896
; Sequence 1896, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1896
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1896

Query Match	70.5%;	Score 949;	DB 3;	Length 245;
Best Local Similarity	73.8%;	Pred. No. 6.1e-64;		
Matches 186;	Conservative 21;	Mismatches 35;	Indels 10;	Gaps 3;
Oy	2	QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVRQAPQGRFEWGMWINPYNGNKEF	61	
Db	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPQGRLEWGMWINAGNNTKY	60	
Oy	62	SAKFQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGEWGMWDDSPDNYMDVWGKG	121	
Db	61	SKQFGQRTTITRDTTSASTAYMELSLRSADTAVVYCARVGEWGMWDDSPDNYMDVWGQG	113	
Oy	122	TTVIVSSGGSGSGSGSGSGSGSDIE--LTQSPGTLISLSPGERATFSCRSSHSIRSRVAV	179	
Db	114	TMVTVSSGGSGSGSGSGSGSGSALETTLTQSPGTLISLSPGERATLSCRAQASGNYLAW	173	
Oy	180	YQKPGQAPRLVHGVSNRAGISDRPSGSGSGDFTLTITRVPEDFALVYCOVYGASS	239	
Db	174	YQKPGQPPSLIIVGASRAIYIPDRFSASGSGDFTLTISRLEPEDFAYVYCOQYG--SS	232	
Oy	240	YTFQGQTKLERK 251		

Db 233 ITFGQGTRELEIK 244

RESULT 2

US-10-293-418-1896
; Sequence 1896, Application US/10293418
; Publication No. US20030223996A1

GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys

; FILE REFERENCE: PF523P2

; CURRENT APPLICATION NUMBER: US/10/293,418

; PRIOR FILING DATE: 2002-11-27

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1896

; LENGTH: 245

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-418-1896

Query Match 70.5%; Score 949; DB 4; Length 245;

Best Local Similarity 73.8%; Pred. No. 6.1e-64;

Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOASGYRFSNFTVHVRQAPGQRFEMWGINPYNKNKEF 61

Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRFLEWGWINAGNGNTKY 60

Qy 62 SAKFDQRTVFTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVMGKG 121

Db 61 SQKFGQRTVITRTDSASTAYMELSLRSRSEDATVYYCAREG-----PGYYGMDVMGQG 113

Qy 122 TTVIVSSGGGGSGGGGGGGSDIE--LTQSPGTLSPGGERATFSCRSHSIRSRVAV 179

Db 114 TMVTIVSSGGGGSGGGGGGGSALETTLTQSPGTLSPGGERATLSCRASQAIGSNYLAW 173

Qy 180 YQHKGQAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDEALYYCQVYGASS 239

Db 174 YQKQFGQPPSLIYGASSRATGIPDRFSASGSGTDFTLTISRLEPEDEAVYYCQYQG-SS 232

Qy 240 YTFGGQTKLERK 251

Db 233 ITFGQGTRELEIK 244

RESULT 3

US-10-322-673-56

; Sequence 56, Application US/10322673

; Publication No. US20030180296A1

GENERAL INFORMATION:

; APPLICANT: Salcedo et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

; FILE REFERENCE: PF595

; CURRENT APPLICATION NUMBER: US/10/322,673

; CURRENT FILING DATE: 2002-12-19

; PRIOR APPLICATION NUMBER: 60/341,237

; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-322-673-56

Query Match 67.6%; Score 910; DB 4; Length 247;
Best Local Similarity 69.4%; Pred. No. 5.5e-61;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOASGYRFSNFTVHVRQAPGQRFEMWGINPYNKNKEF 61

Db 1 EVQLVQSGAEVKKPGASVKVSCTASGYTFTSYGITVWRQAPGQGLEWGWISAYNGKNTY 60

Qy 62 SAKFDQRTVFTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNY---YMDVM 118

Db 61 VQELQGRVTMTDTSTSTVYMWELTSLRSDDTAVVYCARRG-----NNYRFGYDFEW 111

Qy 119 KGTTIVSSGGGGSGGGGGGGSDIE--LTQSPGTLSPGGERATFSCRSHSIRSR 176

Db 112 GQGTIVTVSSGGGGSGGGGGGGSALETTLTQSPGTLSPGGERATLSCRASQSISSN 171

Qy 177 VANYQHKGQAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDEALYYCQVYG 236

Db 172 LAMVYQKQPGAPRLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEAEDFAVYYCQYQG 231

Qy 237 ASSYTFGGQTKLERK 251

Db 232 SSPITFGQGTRELEIK 246

RESULT 4

US-10-981-465-56

; Sequence 56, Application US/10981465

; Publication No. US20050214205A1

GENERAL INFORMATION:

; APPLICANT: Salcedo et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

; FILE REFERENCE: PF585P1

; CURRENT APPLICATION NUMBER: US/10/981,465

; CURRENT FILING DATE: 2004-11-05

; PRIOR APPLICATION NUMBER: 60/608,386

; PRIOR FILING DATE: 2004-09-10

; PRIOR APPLICATION NUMBER: PCT/US04/013900

; PRIOR FILING DATE: 2004-05-05

; PRIOR APPLICATION NUMBER: 60/468,092

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/495,140

; PRIOR FILING DATE: 2003-08-15

; PRIOR APPLICATION NUMBER: 10/322,673

; PRIOR FILING DATE: 2002-12-19

; PRIOR APPLICATION NUMBER: 60/369,877

; PRIOR FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 60/384,828

; PRIOR FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: 60/396,591

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/403,370

```
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-465-56

Query Match      67.6%; Score 910; DB 5; Length 247;
Best Local Similarity 69.4%; Pred. No. 5.5e-61;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy  2 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPQGFQFVWGWNPYNGNKEF 61
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 EVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPQGFQFVWGWNPYNGNKEF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNY---YMDVM 118
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 VQELQGRVTMTDTSSTVYMWELTSLRSDDTAVVYCARG-----NNYRFGYDFW 111
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  119 GKGTIVVSSGGSGGGSGGGGGGSDIE--LTQSPGTLSPGGERATFSCRSHSIRSR 176
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  112 GQGLTVTVSSGGSGGGSGGGGGGSALETTLTQSPGTLSPGGERATLSCRASQSISSN 171
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  177 VANYQHFGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVPEPDPALYYCQVYG 236
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  172 LAMTQQKPGRAPRLIYGCASSRAIGIPDRFSGSGGTDFTLTISRLEAEDFVAVYCCQYG 231
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  237 ASSYTFGGGTGLERK 251
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  232 SSPITFGGQTRLEIK 246
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-10-981-621-56
; Sequence 56, Application US/10981621
; Publication No. US20050214206A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1D1
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-673-56
```

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-621-56

Query Match      67.6%; Score 910; DB 5; Length 247;
Best Local Similarity 69.4%; Pred. No. 5.5e-61;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy  2 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPQGFQFVWGWNPYNGNKEF 61
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 EVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPQGFQFVWGWNPYNGNKEF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNY---YMDVM 118
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 VQELQGRVTMTDTSSTVYMWELTSLRSDDTAVVYCARG-----NNYRFGYDFW 111
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  119 GKGTIVVSSGGSGGGSGGGGGGSDIE--LTQSPGTLSPGGERATFSCRSHSIRSR 176
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  112 GQGLTVTVSSGGSGGGSGGGGGGSALETTLTQSPGTLSPGGERATLSCRASQSISSN 171
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  177 VANYQHFGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVPEPDPALYYCQVYG 236
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  172 LAMTQQKPGRAPRLIYGCASSRAIGIPDRFSGSGGTDFTLTISRLEAEDFVAVYCCQYG 231
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  237 ASSYTFGGGTGLERK 251
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  232 SSPITFGGQTRLEIK 246
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-10-981-673-56
; Sequence 56, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1D2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-673-56

Query Match      67.6%; Score 910; DB 5; Length 247;
```



```
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-12
```

```
Query Match 65.6%; Score 884; DB 3; Length 251;
Best Local Similarity 68.4%; Pred. No. 5.2e-59;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRAQPGQRFEMWGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKPGASVKVCKASGYTFSNHGISWVRQAPGQGLEWVWISGHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AQKFGQGRVTMTADTSTSTAYIELSLKSDDDTAVYYCARP---FYDTLTRYVYFQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
Db 118 GTMTVTVSSGGGGSGGGSGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHKPGQAPRLVTHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEPFALYYCOVYGAS 238
Db 178 WYQKPGQAPRLMYGASRRATGVPDRFSGSGSGTDFTLTISRLEPEFAVYYCOQYATS 237

Qy 239 SYTFGGQTGLERK 251
Db 238 PRTEGGQTRLEIK 250
```

```
RESULT 10
US-09-880-748-26
; Sequence 26, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 251
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-26

Query Match 65.6%; Score 884; DB 3; Length 251;
Best Local Similarity 68.4%; Pred. No. 5.2e-59;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRAQPGQRFEMWGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKPGASVKVCKASGYTFSNHGISWVRQAPGQGLEWVWISGHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AQKFGQGRVTMTADTSTSTAYIELSLKSDDDTAVYYCARP---FYDTLTRYVYFQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
Db 118 GTMTVTVSSGGGGSGGGSGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHKPGQAPRLVTHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEPFALYYCOVYGAS 238
Db 178 WYQKPGQAPRLMYGASRRATGVPDRFSGSGSGTDFTLTISRLEPEFAVYYCOQYATS 237

Qy 239 SYTFGGQTGLERK 251
Db 238 PRTEGGQTRLEIK 250
```

```
RESULT 11
US-10-293-418-12
; Sequence 12, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-12
```

```
Query Match 65.6%; Score 884; DB 4; Length 251;
Best Local Similarity 68.4%; Pred. No. 5.2e-59;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRAQPGQRFEMWGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKPGASVKVCKASGYTFSNHGISWVRQAPGQGLEWVWISGHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AQKFGQGRVTMTADTSTSTAYIELSLKSDDDTAVYYCARP---FYDTLTRYVYFQYFDHWGQ 117
```

US-09-880-748-22
; Sequence 22, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-22

Query Match 65.6%; Score 883; DB 3; Length 251;
Best Local Similarity 68.4%; Pred. No. 6.2e-59;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRFQFWMGWNPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFNHNHGISWVRQAPGQGLEWGWISGHDDSTKY 60

Qy 62 SAKFDQRTVFTADTSANTAYMELRSLSADTAVVYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AOKFQGRVTMTADTSTSTAYIELRLSKSDDTAVVYCARP---FYDTLTRYVQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSRRA 178
Db 118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHPGQAPRLVIHGVSNRAGISDRFSGSGGTDFLTITRVEPEFALYVCQVYGAS 238
Db 178 WYQKPGQAPRLMYGASRRATGVPDRFSGSGGTDFLTITSLRLEPEDFAVYICQYATS 237

Qy 239 SYTFGGQTKLERK 251
Db 238 PRTEGGQTRLEIK 250

RESULT 14
US-09-880-748-28
; Sequence 28, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239

US-10-293-418-26
; Sequence 26, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 26
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-26

Query Match 65.6%; Score 884; DB 4; Length 251;
Best Local Similarity 68.4%; Pred. No. 5.2e-59;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRFQFWMGWNPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFNHNHGISWVRQAPGQGLEWGWISGHDDSTKY 60

Qy 62 SAKFDQRTVFTADTSANTAYMELRSLSADTAVVYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AOKFQGRVTMTADTSTSTAYIELRLSKSDDTAVVYCARP---FYDTLTRYVQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSRRA 178
Db 118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHPGQAPRLVIHGVSNRAGISDRFSGSGGTDFLTITRVEPEFALYVCQVYGAS 238
Db 178 WYQKPGQAPRLMYGASRRATGVPDRFSGSGGTDFLTITSLRLEPEDFAVYICQYATS 237

Qy 239 SYTFGGQTKLERK 251
Db 238 PRTEGGQTRLEIK 250

RESULT 13

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-28

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Query Match 65.6%; Score 883; DB 3; Length 251;
Best Local Similarity 67.2%; Pred. No. 6.2e-59;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

Search completed: March 20, 2006, 07:49:20
Job time : 70 secs

RESULT 15

US-09-880-748-33
; Sequence 33, Application US/09880748
; Publication No. US20030059937A1

Query Match	65.6%;	Score 883;	DB 3;	Length 251;
Best Local Similarity	67.2%;	Pred. No. 6.2e-59;		
Matches 174;	Conservative	27;	Mismatches 40;	Indels 18;
				Gaps 4;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:47:04 ; Search time 27 seconds
(without alignments)
768.578 Million cell updates/sec

Title: US-09-673-707-1

Perfect score: 1347
Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYGASSYFGQGTGLR 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	800.5	59.4	269	2	US-08-646-265A-109
2	797	59.2	288	2	US-09-423-439-38
3	797	59.2	673	2	US-09-423-439-32
4	786	58.4	267	2	US-09-485-737B-2
5	786	58.4	267	2	US-10-071-485-2
6	786	58.4	541	2	US-09-485-737B-85
7	786	58.4	541	2	US-10-071-485-85
8	786	58.4	711	2	US-09-485-737B-90
9	786	58.4	711	2	US-10-071-485-90
10	770	57.2	240	1	US-08-488-113B-148
11	770	57.2	240	1	US-08-477-484B-148
12	770	57.2	240	1	US-08-646-360-148
13	770	57.2	240	2	US-08-839-765-148
14	770	57.2	240	2	US-09-136-389-148
15	770	57.2	240	2	US-09-610-838-148
16	770	57.2	240	2	US-09-711-485-148
17	760	56.4	244	1	US-08-553-497A-20
18	756.5	56.2	297	2	US-09-486-814A-2
19	755	56.1	249	1	US-08-797-689-18
20	755	56.1	249	1	US-09-984-186-18
21	753.5	55.9	240	1	US-08-800-198-8
22	753.5	55.9	240	2	US-09-296-595-8
23	752.5	55.9	599	1	US-08-463-163-3
24	749.5	55.6	256	2	US-09-526-738A-2
25	749.5	55.6	258	2	US-09-526-738A-4
26	747.5	55.5	239	2	US-08-279-772A-8
27	747.5	55.5	239	2	US-08-902-486-11

28	746.5	55.4	270	1	US-08-652-507-2	Sequence 2, Appli
29	746	55.4	246	1	US-08-553-497A-24	Sequence 24, Appl
30	745.5	55.3	240	2	US-09-485-737B-91	Sequence 91, Appl
31	745.5	55.3	240	2	US-10-071-485-91	Sequence 91, Appl
32	745.5	55.3	249	2	US-09-297-181-4	Sequence 4, Appli
33	743	55.2	244	1	US-08-553-497A-22	Sequence 22, Appl
34	742	55.1	238	2	US-09-798-689-21	Sequence 21, Appl
35	741.5	55.0	530	2	US-08-840-713-2	Sequence 2, Appli
36	741.5	55.0	615	2	US-08-840-713-35	Sequence 35, Appl
37	741.5	55.0	617	2	US-08-840-713-37	Sequence 37, Appl
38	740.5	55.0	553	1	US-08-661-052-16	Sequence 16, Appl
39	740.5	55.0	553	2	US-08-188-082-16	Sequence 16, Appl
40	740.5	55.0	553	2	US-09-364-088-16	Sequence 16, Appl
41	740.5	55.0	553	2	US-09-102-716-16	Sequence 16, Appl
42	739.5	54.9	637	1	US-08-235-838-14	Sequence 14, Appl
43	739.5	54.9	637	1	US-08-235-838-16	Sequence 14, Appl
44	739.5	54.9	637	1	US-08-465-473B-14	Sequence 14, Appl
45	739.5	54.9	637	1	US-08-465-473B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-646-265A-109
; Sequence 109, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-265A-109

Query Match 59.4%; Score 800.5; DB 2; Length 269;

Best Local Similarity 61.1%; Pred. No. 2e-61;
Matches 154; Conservative 31; Mismatches 52; Indels 15; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGMINPYGNKEF 61
Db 23 QVQLVQSGAEVKKPGSSVKVSCKASGPNKIDTYIHVRQAPGQGLEWMGRIDPADGNTKY 82

Qy 62 SAKFDQRTVTTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSPQDNYM--DVWG 119
Db 83 DPKFQGRVTTTADSTNTAYMELSSLSRSEDATFYFCASA-----YYVNQDYWG 130

Qy 120 KGTTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179
Db 131 QGITVTVSSGGGGGGGGGGSDIQMTQSPSLASVGDRTTITCKASQNV-GTNVAV 189

Qy 180 YQHPKGPAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGASS 239
Db 190 YQKPGKAPKPLIYASVRYSGVPSRFSFGSGSGTDFTLTISLQPEDIATYYCQYNSYP 249

Qy 240 YTFGQGTKLK 251
Db 250 RAFQGGTKVEIK 261

RESULT 2

US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match 59.2%; Score 797; DB 2; Length 288;
Best Local Similarity 58.1%; Pred. No. 4.4e-61;
Matches 150; Conservative 43; Mismatches 47; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGMINPYGNKEF 61
Db 23 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGMINPYGNKEF 82

Qy 62 SAKFDQRTVTTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSPQDNYMVDVWGK 121

Db 83 NEFKNKATLTVDKSTTAYMQLSSLTSEDSAVYYCARERAYGDDA-----MDYWGQG 136

Qy 122 TTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHI-----RSRR 176
Db 137 TTVTVSSGGGGGGGGGGSDIELSQSPSLAVSAGEKVTMSCKSSQSLNSRTRKNY 196

Qy 177 VAWYQHPKGPAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYG 236
Db 197 LAWYQQRPGQSPKLLIYWASTRTSGVPDRFTGSGSGTDFTLTISVQAEDLAIYYCK--- 253

Qy 237 ASSY---TFGQGTKLK 251
Db 254 -QSYTLRTFGGTKLEIK 270

RESULT 3

US-09-423-439-32
; Sequence 32, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

Query Match 59.2%; Score 797; DB 2; Length 673;
Best Local Similarity 58.1%; Pred. No. 1.2e-60;
Matches 150; Conservative 43; Mismatches 47; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGMINPYGNKEF 61
Db 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGMINPYGNKEF 79

Qy 62 SAKFDQRTVTTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSPQDNYMVDVWGK 121
Db 80 NEFKNKATLTVDKSTTAYMQLSSLTSEDSAVYYCARERAYGDDA-----MDYWGQG 133

Qy 122 TTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHI-----RSRR 176
Db 134 TTVTVSSGGGGGGGGGGSDIELSQSPSLAVSAGEKVTMSCKSSQSLNSRTRKNY 193

Qy 177 VAWYQHPKGPAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYG 236

Db 194 LAWYQORPGQSKLLIYWASTRTSGVDRFTGSGSGTDFTLTISVQAEADLAIYCK--- 250
Qy 237 ASSY---TFGQGTLEIK 251
Db 251 -QSYTLRTFGGTKLEIK 267

RESULT 4
US-09-485-737B-2
; Sequence 2, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-485-737B-2

Query Match 58.4%; Score 786; DB 2; Length 267;
Best Local Similarity 58.8%; Pred. No. 3.6e-60;
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRPFWGWINPYNGNKEF 61
Db 23 QVQLVQSGSELKPKGASVKISCKASGYTFTDYGNNWVKQAPGQGLKWMGWINTYTGSTY 82
Qy 62 SAKFDQRTVTADTTSANTAYMELRLSADTAVYCARVGEWGWDDSPQDNYMDVWGKG 121
Db 83 VDDFKGRFVSLDTSVAAYLIQISLKAEDTATYFCARRG-----FYAMDYWGQG 132
Qy 122 TTIVTSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAVYQ 181
Db 133 TTVTVSSGGGGGGGGGGSDIVLTQSPATMSASPGERVLTLCSSASSI--SYMPFWYH 190
Qy 182 HKPGQAPRLVHGVSNRAGISDRFSGSGGTDFTLITRVEPDPFALYVCQVYGASST 241
Db 191 QRPQSPRLIYDTSNLASGVPARFSGSGGTSTYSLTISRMEPDPFATYFCHQSSSYPT 250
Qy 242 FGGQTKLERK 251
Db 251 FGGQTKLEIK 260

RESULT 5
US-10-071-485-2
; Sequence 2, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK, CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485

; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-071-485-2

Query Match 58.4%; Score 786; DB 2; Length 267;
Best Local Similarity 58.8%; Pred. No. 3.6e-60;
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRPFWGWINPYNGNKEF 61
Db 23 QVQLVQSGSELKPKGASVKISCKASGYTFTDYGNNWVKQAPGQGLKWMGWINTYTGSTY 82
Qy 62 SAKFDQRTVTADTTSANTAYMELRLSADTAVYCARVGEWGWDDSPQDNYMDVWGKG 121
Db 83 VDDFKGRFVSLDTSVAAYLIQISLKAEDTATYFCARRG-----FYAMDYWGQG 132
Qy 122 TTIVTSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAVYQ 181
Db 133 TTVTVSSGGGGGGGGGGSDIVLTQSPATMSASPGERVLTLCSSASSI--SYMPFWYH 190
Qy 182 HKPGQAPRLVHGVSNRAGISDRFSGSGGTDFTLITRVEPDPFALYVCQVYGASST 241
Db 191 QRPQSPRLIYDTSNLASGVPARFSGSGGTSTYSLTISRMEPDPFATYFCHQSSSYPT 250
Qy 242 FGGQTKLERK 251
Db 251 FGGQTKLEIK 260

RESULT 6
US-09-485-737B-85
; Sequence 85, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-85

Query Match 58.4%; Score 786; DB 2; Length 541;

Db 169 QRPQSPRLIYDTSNLASGVPARFSGSGTYSYLSLTISRMEPEDFATYFCHQSSSYPT 228

QY 242 FGQGTKLERK 251

Db 229 FGQGTKLEIK 238

RESULT 8

US-09-485-737B-90

; Sequence 90, Application US/09485737B

; Patent No. 6350860

; GENERAL INFORMATION:

; APPLICANT: Buysee, Marie-Ange

; APPLICANT: Sablon, Erwin

; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,

; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

; FILE REFERENCE: INNS:015

; CURRENT APPLICATION NUMBER: US/09/485,737B

; CURRENT FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: PCT/EP 98/05165

; PRIOR FILING DATE: 1998-08-14

; PRIOR APPLICATION NUMBER: EPO 98870139.7

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: EPO 97870122.5

; PRIOR FILING DATE: 1997-08-18

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 90

; LENGTH: 711

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: SYNTHETIC

US-09-485-737B-90

Query Match 58.4%; Score 786; DB 2; Length 711;

Best Local Similarity 58.8%; Pred. No. 1.1e-59;

Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

QY 2 QVQLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFQFWMGWINPYGNKEF 61

Db 473 QVQLVQSGSELKPKGASVKISKASGYTFDYGNNVVKQAPGQGLKMWGINTYTGESY 532

QY 62 SAKFQDRVTFTADTSANTAYMELRSADTAVYICARVGEWGWDDSPQDNYMDVMGKG 121

Db 533 VDDFKGRFVSLDTSVAAYLIQISLKAEDTATYFCARRG-----FYAMDYWGQG 582

QY 122 TTVTVSSGGSGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHRSRRVAWYQ 181

Db 583 TTVTVSSGGSGGGGGGSDIVLTQSPATMSASGERVLTCSASSSI--SYMFWYH 640

QY 182 HKPGQAPRLVTHGVSNRASGISDRFSGSGGTDFLTITRVEPEDFALYYCOVYGASSYT 241

Db 641 QRPQSPRLIYDTSNLASGVPARFSGSGTYSYLSLTISRMEPEDFATYFCHQSSSYPT 700

QY 242 FGQGTKLERK 251

Db 701 FGQGTKLEIK 710

RESULT 9

US-10-071-485-90

; Sequence 90, Application US/10071485

; Patent No. 6830752

; GENERAL INFORMATION:

; APPLICANT: Buysee, Marie-Ange

; APPLICANT: Sablon, Erwin

; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC

; TITLE OF INVENTION: SHOCK,

; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

; FILE REFERENCE: INNS:015

; CURRENT APPLICATION NUMBER: US/10/071,485

; CURRENT FILING DATE: 2002-02-07

Best Local Similarity 58.8%; Pred. No. 8.3e-60;

Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

QY 2 QVQLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFQFWMGWINPYGNKEF 61

Db 1 QVQLVQSGSELKPKGASVKISKASGYTFDYGNNVVKQAPGQGLKMWGINTYTGESY 60

QY 62 SAKFQDRVTFTADTSANTAYMELRSADTAVYICARVGEWGWDDSPQDNYMDVMGKG 121

Db 61 VDDFKGRFVSLDTSVAAYLIQISLKAEDTATYFCARRG-----FYAMDYWGQG 110

QY 122 TTVTVSSGGSGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHRSRRVAWYQ 181

Db 111 TTVTVSSGGSGGGGGGSDIVLTQSPATMSASGERVLTCSASSSI--SYMFWYH 168

QY 182 HKPGQAPRLVTHGVSNRASGISDRFSGSGGTDFLTITRVEPEDFALYYCOVYGASSYT 241

Db 169 QRPQSPRLIYDTSNLASGVPARFSGSGTYSYLSLTISRMEPEDFATYFCHQSSSYPT 228

QY 242 FGQGTKLERK 251

Db 229 FGQGTKLEIK 238

RESULT 7

US-10-071-485-85

; Sequence 85, Application US/10071485

; Patent No. 6830752

; GENERAL INFORMATION:

; APPLICANT: Buysee, Marie-Ange

; APPLICANT: Sablon, Erwin

; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC

; TITLE OF INVENTION: SHOCK,

; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

; FILE REFERENCE: INNS:015

; CURRENT APPLICATION NUMBER: US/10/071,485

; CURRENT FILING DATE: 2002-02-07

; PRIOR APPLICATION NUMBER: 09/485,737

; PRIOR FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: PCT/EP 98/05165

; PRIOR FILING DATE: 1998-08-14

; PRIOR APPLICATION NUMBER: EPO 98870139.7

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: EPO 97870122.5

; PRIOR FILING DATE: 1997-08-18

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 85

; LENGTH: 541

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: SYNTHETIC

US-10-071-485-85

Query Match 58.4%; Score 786; DB 2; Length 541;

Best Local Similarity 58.8%; Pred. No. 8.3e-60;

Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

QY 2 QVQLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFQFWMGWINPYGNKEF 61

Db 1 QVQLVQSGSELKPKGASVKISKASGYTFDYGNNVVKQAPGQGLKMWGINTYTGESY 60

QY 62 SAKFQDRVTFTADTSANTAYMELRSADTAVYICARVGEWGWDDSPQDNYMDVMGKG 121

Db 61 VDDFKGRFVSLDTSVAAYLIQISLKAEDTATYFCARRG-----FYAMDYWGQG 110

QY 122 TTVTVSSGGSGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHRSRRVAWYQ 181

Db 111 TTVTVSSGGSGGGGGGSDIVLTQSPATMSASGERVLTCSASSSI--SYMFWYH 168

QY 182 HKPGQAPRLVTHGVSNRASGISDRFSGSGGTDFLTITRVEPEDFALYYCOVYGASSYT 241

PRIOR APPLICATION NUMBER: 09/485,737
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: 711
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match 58.4%; Score 786; DB 2; Length 711;
Best Local Similarity 58.8%; Pred. No. 1.1e-59;
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;
QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRFENWGMINPYNGNKEF 61
DB 473 QVQLVQSGSELKPKGASVKISCKASGYTFTDYGNNVYKQAPGQGLKRWGINTYTGESTY 532
QY 62 SAKFQDRTVFTADTSANTAYMELRSASDTAVYVCARVGEWGWDDSPQDNYMDVWGKG 121
DB 533 VDFKGRFVSLDTSVAAYLQISLAEADTAITYFCARRG-----FYAMDYWGQG 582
QY 122 TTVIVSSGGGGGGGGGGGGSDIELTQSPGTLSLSPGERATFSCRSRSHSIRSRVAVYQ 181
DB 583 TTVIVSSGGGGGGGGGGGGSDIVLTQSPATMSASPGERVTLTCSASSSI--SYMPWYH 640
QY 182 HKPQAPRLVIHGVSNRNASGISDRFSGSGSGTDFTLTITRVEPDFALYYCOVYGASST 241
DB 641 QRPQSPRLIYDTSNLASGVPARFSGSGSGTSYSLTISRMEPDFAITYFCHOSSYPFT 700
QY 242 FGQGTKLERK 251
DB 701 FGQGTKLEIK 710

RESULT 10
US-08-488-113B-148
Sequence 148, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-148
Query Match 57.2%; Score 770; DB 1; Length 240;
Best Local Similarity 56.4%; Pred. No. 7.6e-59;
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;
QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRFENWGMINPYNGNKEF 61
DB 1 EQLVQSGGGLKPKGASVKISCKASGYTFTYGNWVYKQAPGKGLRWGINTYTGESTY 60
QY 62 SAKFQDRTVFTADTSANTAYMELRSASDTAVYVCARVGEWGWDDSPQDNYMDVWGKG 121
DB 61 ADSFKGRFTFSLDDSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVMGQG 111
QY 122 TTVIVSSGGGGGGGGGGGGSDIELTQSPGTLSLSPGERATFSCRSRSHSIRSRVAVYQ 181
DB 112 TTVIVSSGGGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQDINS-YLSWFG 170
QY 182 HKPQAPRLVIHGVSNRNASGISDRFSGSGSGTDFTLTITRVEPDFALYYCOVYGASST 241
DB 171 QKPGKAPKTLIYRANRLSEGVPRFSGSGSGTDYTLTISLQYEDFGIYCCQYDESPWT 230
QY 242 FGQGTKLERK 251
DB 231 FGQGTKLEMK 240
RESULT 11
US-08-477-484B-148
Sequence 148, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-148

Query Match 57.2%; Score 770; DB 1; Length 240;
Best Local Similarity 56.4%; Pred. No. 7.6e-59;
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

Qy 2 QVQLQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFQFWMGWINPYGNKKEF 61
Db 1 EIQLVQSGGLVKPGSVRIISCAASGYTFYNYGMNVRQAPGKGLWGMWINTHTGEPTY 60

Qy 62 SAKFDQDRVTFTADTSANTAYMELSLRSADTAVYICARVGEWGWDDSPQDNYMDVWGKG 121
Db 61 ADSFKGRFTFLDSDSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111

Qy 122 TTVTVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAVYQ 181
Db 112 TTVTVSSGGGGGGGGGGSDIQMTQSPSLASVGDRTVITCRASQDINS-YLSWFQ 170

Qy 182 HKPGQAPRLVIHGVSNRASGISDRFSGSGGTDTFTLTITRVEPDFALYYCQVYGASST 241
Db 171 QKPKAKPTLIYRANRLSEGVPSRFSFGSGGTDTYLTITSSQLQYEDFGIYYCQYDESPWT 230

Qy 242 FGQGTKLK 251
Db 231 FGGGTKLEMK 240

RESULT 12
US-08-646-360-148
; Sequence 148, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroli, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
;
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-360-148

Query Match 57.2%; Score 770; DB 1; Length 240;
Best Local Similarity 56.4%; Pred. No. 7.6e-59;
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

Qy 2 QVQLQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFQFWMGWINPYGNKKEF 61
Db 1 EIQLVQSGGLVKPGSVRIISCAASGYTFYNYGMNVRQAPGKGLWGMWINTHTGEPTY 60

Qy 62 SAKFDQDRVTFTADTSANTAYMELSLRSADTAVYICARVGEWGWDDSPQDNYMDVWGKG 121
Db 61 ADSFKGRFTFLDSDSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111

Qy 122 TTVTVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAVYQ 181
Db 112 TTVTVSSGGGGGGGGGGSDIQMTQSPSLASVGDRTVITCRASQDINS-YLSWFQ 170

Qy 182 HKPGQAPRLVIHGVSNRASGISDRFSGSGGTDTFTLTITRVEPDFALYYCQVYGASST 241
Db 171 QKPKAKPTLIYRANRLSEGVPSRFSFGSGGTDTYLTITSSQLQYEDFGIYYCQYDESPWT 230

Qy 242 FGQGTKLK 251
Db 231 FGGGTKLEMK 240
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RESULT 13

US-08-839-765-148
; Sequence 148, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-148

Query Match 57.2%; Score 770; DB 2; Length 240;

Best Local Similarity 56.4%; Pred. No. 7.6e-59;

Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEKKGKPGASVKVSCASGYRFSNFTVHWVVRQAPGQRFEMWGHINPYNKGF 61
Db 1 EIQLVQSGGLVLPGGSVRSICASGYTFYTNWVVRQAPGKLEWGWINTHTGPTY 60
Qy 62 SAKFQDVTFTADTSANTAYMELRLSRASDTAVYCARVGEWGWDDSPQDNYMDVWKGK 121
Db 61 ADSFKGFTSLDDSKNTALQLNSLRADTAIVYCTTRG-YDW-----YFDVWVGQ 111
Qy 122 TTVIVSSGGSGGGGGGGSDIELTQSPGRTLSLSPGERATFSCRSHSIRSRVAVYQ 181
Db 112 TTVIVSSGGSGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQDINS-YLSWFQ 170

Qy 182 HKPGQAPRLVHGVSNRASGISDRFSGSGSGTDFLTITTRVEPRDFALYYCOVYGASSYT 241
Db 171 QKFGKAPKTLIYRANRLESQVPSRFSGSGSGTDTLTIISSLOYEDFGIYYCQYDPSWT 230
Qy 242 FGGTKLERK 251
Db 231 FGGTKLEMK 240

RESULT 14

US-09-136-389-148
; Sequence 148, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-136-389-148

Query Match

Best Local Similarity 57.2%; Score 770; DB 2; Length 240;

Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-148

Query Match 57.2%; Score 770; DB 2; Length 240;
Best Local Similarity 56.4%; Pred. No. 7 6e-59;
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

QY 2 QVLEQSGAEVKKPGASVKVSQAQGYRFSNFTVHWVRQAPGQRFQWGMGINPYNGNKEF 61
Db 1 EIQLVQSGGLVKPGGSRVISAASGYTFNYGMNVRQAPGKGLWMGWINHTGPTV 60
QY 62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGDSPQDNYMDVWGK 121
Db 61 ADSFKGRFTFSLDSSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111
QY 122 TTVIVSSGGSGGGGGGGGGDIETQSPGTLSPGERATFSCSSHSIRRRVAVYQ 181
Db 112 TTVIVSSGGSGGGGGGGGGDIQMTQSPSSLSASVGDRTVITCRASQDINS-YLSWFQ 170
QY 182 HKPQAPRLVIHGVSNRASGISDRFSGSGGTDTLTITRVEPEDFALYYCQVYGASSYT 241
Db 171 QKFGKAPKTLIYRANRLESVPSRFSGSGGTDTLTITSLQYEDFGIYYCQYDESPWT 230
QY 242 FGGGTKLERK 251
Db 231 FGGGTKLEMK 240

Search completed: March 20, 2006, 07:47:39
Job time : 27 secs

QY 2 QVLEQSGAEVKKPGASVKVSQAQGYRFSNFTVHWVRQAPGQRFQWGMGINPYNGNKEF 61
Db 1 EIQLVQSGGLVKPGGSRVISAASGYTFNYGMNVRQAPGKGLWMGWINHTGPTV 60
QY 62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGDSPQDNYMDVWGK 121
Db 61 ADSFKGRFTFSLDSSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111
QY 122 TTVIVSSGGSGGGGGGGGGDIETQSPGTLSPGERATFSCSSHSIRRRVAVYQ 181
Db 112 TTVIVSSGGSGGGGGGGGGDIQMTQSPSSLSASVGDRTVITCRASQDINS-YLSWFQ 170
QY 182 HKPQAPRLVIHGVSNRASGISDRFSGSGGTDTLTITRVEPEDFALYYCQVYGASSYT 241
Db 171 QKFGKAPKTLIYRANRLESVPSRFSGSGGTDTLTITSLQYEDFGIYYCQYDESPWT 230
QY 242 FGGGTKLERK 251
Db 231 FGGGTKLEMK 240

RESULT 15
US-09-610-838-148
Sequence 148, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESS: McAndrews, Held & Malloy, Ltd.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:36 ; Search time 75.5 Seconds
(without alignments)
23.278 Million cell updates/sec

Title: US-09-673-707-10

Perfect score: 20

Sequence: 1 REDL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	2	Aar95220 Pseudomon
2	20	100.0	4	2	Aaw76395 Pseudomon
3	20	100.0	4	2	Aaw52263 C-termina
4	20	100.0	4	2	Abb76202 Peptide u
5	20	100.0	4	2	Aaw92910 Pseudomon
6	20	100.0	4	2	Aay49698 Pseudomon
7	20	100.0	4	2	Aay92924 Pseudomon
8	20	100.0	4	4	Aab49323 Endosomal
9	20	100.0	4	5	Aau96732 Human XAG
10	20	100.0	4	5	Aae28524 Endoplasm
11	20	100.0	4	6	Aae33356 Endoplasm
12	20	100.0	4	6	Abri61856 Pseudomon
13	20	100.0	4	7	Adc84561 Carboxyl
14	20	100.0	4	8	Adg5841 Pseudomon
15	20	100.0	4	8	Adn07007 Pseudomon
16	20	100.0	4	8	Adp64378 Carboxyl
17	20	100.0	4	8	Adp79648 Pseudomon
18	20	100.0	4	9	Adz21546 Endoplasm
19	20	100.0	4	9	Aea50149 Pseudomon
20	20	100.0	4	9	Aeb27747 Anti-pros
21	20	100.0	4	9	Aeb31417 Endoplasm
22	20	100.0	5	2	Aar95064 Pseudomon
23	20	100.0	5	2	Aar95221 Pseudomon
24	20	100.0	5	2	Aaw76394 Pseudomon

25	20	100.0	5	2	AAW52260	C-termina
26	20	100.0	5	2	AAW92909	Pseudomon
27	20	100.0	5	2	AAW49697	Pseudomon
28	20	100.0	5	2	AAW92923	Pseudomon
29	20	100.0	5	5	AAE28523	Endoplasm
30	20	100.0	5	6	AAE33355	Endoplasm
31	20	100.0	5	8	ADN07006	Pseudomon
32	20	100.0	5	8	ADZ21545	Endoplasm
33	20	100.0	5	9	AEb27746	Anti-pros
34	20	100.0	6	2	AAW59000	Human HLA
35	20	100.0	6	2	AAW58997	Human HLA
36	20	100.0	6	4	AAAB35209	Retrovira
37	20	100.0	7	2	AAAS0265	Peptide c
38	20	100.0	7	8	ADf94279	Human cel
39	20	100.0	8	2	AAAR43421	La/SSB ep
40	20	100.0	8	2	AAW26557	Soluble p
41	20	100.0	8	4	ABP15821	HIV A24 s
42	20	100.0	8	4	ABP21200	HIV A24 m
43	20	100.0	8	4	ABP24221	HIV A24 m
44	20	100.0	9	3	AAAY66341	HLA-A24-b
45	20	100.0	9	4	AAAB35211	Retrovira
46	20	100.0	9	9	AEb87899	Klebsiell
47	20	100.0	9	9	AEb87903	G. stearo
48	20	100.0	9	9	AEb87895	Pseudomon
49	20	100.0	10	2	AAAR41212	Peptide f
50	20	100.0	10	2	AAAR83075	HLA-B2702
51	20	100.0	10	2	AAAR83094	HLA-B2702
52	20	100.0	10	2	AAAR95425	HLA-B2702
53	20	100.0	10	2	AAAR95423	HLA-B2705
54	20	100.0	10	2	AAW07513	T-cell mo
55	20	100.0	10	2	AAW41477	Fragment
56	20	100.0	10	2	AAW47271	Immunomod
57	20	100.0	10	2	AAW47269	Immunomod
58	20	100.0	10	2	AAW33785	Peptide B
59	20	100.0	10	2	AAW33787	Peptide B
60	20	100.0	10	4	AAAY72488	Immunosup
61	20	100.0	11	6	ABU60645	Human met
62	20	100.0	11	8	ADH08133	Human ADA
63	20	100.0	12	3	AAAB14211	Horse cyt
64	20	100.0	12	6	ADA77726	Peptic pe
65	20	100.0	13	2	AAAR13625	Peptide f
66	20	100.0	14	2	AAW26563	Immunogen
67	20	100.0	14	2	AAW76392	Pseudomon
68	20	100.0	14	2	AAAY06083	Bovine ac
69	20	100.0	14	2	AAAY33212	DAR1 deri
70	20	100.0	14	4	AAAB59407	Human Cla
71	20	100.0	14	6	ADA77727	Peptic pe
72	20	100.0	14	6	ADA77724	Peptic pe
73	20	100.0	14	6	ADA77711	Peptic pe
74	20	100.0	15	3	AAAR06573	Bovine cy
75	20	100.0	15	3	AAAY79382	Human ATP
76	20	100.0	15	8	ADM96212	Wild type
77	20	100.0	15	9	ADV22374	HIV-1 Pol
78	20	100.0	16	2	AAAR50266	HLA B27 h
79	20	100.0	16	2	AAW26556	Soluble p
80	20	100.0	16	6	ADA77725	Peptic pe
81	20	100.0	17	2	AAAR71442	Human HLA
82	20	100.0	17	2	AAAR71443	Human [Ph
83	20	100.0	18	2	AAW42876	Sequence
84	20	100.0	19	7	AAU00634	Human mem
85	20	100.0	19	4	ADB88777	Membrane
86	20	100.0	19	8	ABG75428	Membrane
87	20	100.0	20	4	AAAM19911	Peptide #
88	20	100.0	20	4	ABB39884	Peptide #
89	20	100.0	20	4	AAAM33495	Peptide #
90	20	100.0	20	4	ABB24461	Protein #
91	20	100.0	20	4	AAW73294	Human bon
92	20	100.0	20	4	AAAM60623	Human bra
93	20	100.0	20	4	ABG55009	Human liv
94	20	100.0	20	5	ABG43145	Human pep
95	20	100.0	20	6	ABP70216	Amino aci
96	20	100.0	20	9	ADZ98085	Human ami
97	20	100.0	21	6	ABR81775	HPV cp45

98	20	100.0	21	6	ABR81774	Abx81774	HPiV3 WT	XX	WO9613594-A1.
99	20	100.0	21	9	ADW01026	Adw01026	Amino aci	XX	09-MAY-1996.
100	20	100.0	21	9	ADW01025	Adw01025	Amino aci	XX	26-OCT-1995; 95WO-US013811.
101	20	100.0	22	4	AAR14038	Aar14038	Peptide f	XX	28-OCT-1994; 94US-00331396.
102	20	100.0	22	4	AAB50139	Aab50139	Human bra	XX	28-OCT-1994; 94US-00331397.
103	20	100.0	22	8	ADW96211	Adw96211	Wild type	PF	28-OCT-1994; 94US-00331398.
104	20	100.0	23	2	AAR11460	Aar11460	Pseudomon	XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
105	20	100.0	23	2	AAW52266	Aaw52266	C-termina	PR	Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;
106	20	100.0	23	8	ABO58916	Abos8916	Human gen	XX	Fitzgerald D, Brinkmann U, Pai I;
107	20	100.0	25	2	AAR41221	Aar41221	Peptide f	XX	WPI; 1996-251462/25.
108	20	100.0	25	2	AAR83091	Aar83091	HLA-B2702	XX	Single chain fusion proteins and antibodies - useful to diagnose and
109	20	100.0	25	2	AAR95417	Aar95417	HLA-B2705	PA	treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.
110	20	100.0	26	2	AAR83099	Aar83099	Modified	XX	Disclosure; Page 14; 116pp; English.
111	20	100.0	27	2	AAW76393	Aaw76393	ETA-omega	PI	A novel recombinant DNA molecule which encodes a single chain fusion
112	20	100.0	28	4	AAM17802	Aam17802	Peptide #	PI	protein or antibody comprising the Fv region of both the light and heavy
113	20	100.0	28	4	ABB36826	Abb36826	Peptide #	XX	chains of an antibody (Ab) fused together, and an effector molecule,
114	20	100.0	28	4	AAM30311	Aam30311	Peptide #	XX	where the fusion protein or Ab has the binding specificity of monoclonal
115	20	100.0	28	4	ABB28873	Abb28873	Peptide #	CC	Ab (MAB) B1, B3 or B5, can be used for the production of such fusion
116	20	100.0	28	4	ABB31607	Abb31607	Protein #	CC	proteins or antibodies. The fusion proteins can be used in compositions
117	20	100.0	28	4	ABB22149	Abb22149	Human bon	CC	as an immunotoxin to inhibit tumour cell growth. The single chain
118	20	100.0	28	4	AAW69971	Aaw69971	Human bon	CC	antibody can be used to detect the presence or absence of cells bearing a
119	20	100.0	28	4	AAM67213	Aam67213	Human bon	XX	Lewis(Y) carbohydrate antigen in a patient. The antibodies are also
120	20	100.0	28	4	AAW54830	Aaw54830	Human bra	CC	useful as multiple targeting moieties, providing at least 2 kinds of
121	20	100.0	28	4	AAW57568	Aaw57568	Human bra	CC	biological activity. They can also be used in diagnostic assays and for
122	20	100.0	28	4	ABG51671	Abg51671	Human liv	CC	the imaging of tumours when attached to a radiolabel and for the
123	20	100.0	28	4	AAW05449	Aaw05449	Peptide #	CC	pathological diagnosis of tumours. Humanised antibodies are less
124	20	100.0	28	5	ABG39603	Abg39603	Human pep	CC	immunogenic than the mouse MAb5 B1, B3 and B5, making them more suitable
125	20	100.0	28	8	ADT39248	Adt39248	hSARS vir	CC	for long term treatment. The effector molecule used is preferably a drug
126	20	100.0	28	8	ADT39248	Adt39248	hSARS vir	CC	or cytotoxin which then produces an immunotoxin capable of selectively
127	20	100.0	28	8	ADT36778	Adt36778	SARS coro	CC	killing particular cells. Preferred toxins are the Pseudomonas exotoxin
128	20	100.0	28	8	ABY00280	Abby00280	SARS coro	CC	or Diphtheria toxin. These are both highly toxic compounds and so are
129	20	100.0	31	3	AAB20891	Aab20891	Porcine L	CC	modified to eliminate domain Ia of the Pseudomonas toxin, various amino
130	20	100.0	32	9	ADV32651	Adv32651	Hedgehog	CC	acid deletions in domains II and III, single amino acid substitutions and
131	20	100.0	32	9	ADW65057	Adw65057	C. pneumo	CC	addition of one or more sequences at the C-terminal end. The wild type C-
132	20	100.0	35	3	AAW86403	Aaw86403	Human gen	CC	terminal sequence of the Pseudomonas exotoxin is given in AAR95221
133	20	100.0	35	6	ABO53550	Abos3550	Novel hum	XX	Sequence 4 AA;
134	20	100.0	36	4	AAO00161	Aao00161	Human pol	XX	Query Match 100.0%; Score 20; DB 2; Length 4;
135	20	100.0	36	9	ABE84812	Aeb84812	Rice cyst	XX	Best Local Similarity 100.0%; Pred. No. 2e+06;
136	20	100.0	37	5	AAO18561	Aao18561	Nucleic a	XX	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
137	20	100.0	39	4	AAM18489	Aam18489	Peptide #	QY	1 REDL 4
138	20	100.0	39	4	ABB37533	Abb37533	Peptide #	Db	1 REDL 4
139	20	100.0	39	4	AAW58190	Aaw58190	Human bra	RESULT 2	
140	20	100.0	39	4	AAW06078	Aaw06078	Peptide #	AAW76395	
141	20	100.0	39	5	ABG40331	Abg40331	Human pep	XX	AAW76395;
142	20	100.0	40	4	AAU02107	Aau02107	Human fish	XX	11-JAN-1999 (first entry)
143	20	100.0	43	4	ABG00440	Abg00440	Novel hum	XX	Pseudomonas aeruginosa exotoxin A C-terminal motif.
144	20	100.0	44	5	ABP42973	Abp42973	Human ova	DE	Exotoxin A; ETA; drug delivery; membrane transport.
145	20	100.0	45	2	AAW12840	Aaw12840	Human 5'	XX	Pseudomonas aeruginosa.
146	20	100.0	45	4	ABB44517	Abb44517	Peptide #	XX	WO9842876-A1.
147	20	100.0	45	4	ABB27346	Abb27346	Protein #	XX	
148	20	100.0	45	4	AAW78318	Aaw78318	Human bon	XX	
149	20	100.0	45	4	ABG59926	Abg59926	Human liv	XX	
150	20	100.0	46	4	AAW91929	Aaw91929	Human dig	XX	

ALIGNMENTS

RESULT 1
AAR95220
ID AAR95220 standard; protein; 4 AA.
XX
AC AAR95220;
XX
XX 16-DEC-1996 (first entry)
XX
DE Pseudomonas exotoxin modified C-terminal sequence.
XX
XX Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
KW detection; imaging; immunotoxin; targeting; assay; immunoassay;
KW Lewis(Y) carbohydrate antigen.
XX
OS Pseudomonas sp.

PD 01-OCT-1998.
 XX
 PF 24-MAR-1998; 98WO-US005710.
 XX
 PR 26-MAR-1997; 97US-0042056P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Draper RK;
 XX
 DR WPI; 1998-532023/45.
 XX
 PT Delivering compounds to cells as new conjugate with detoxified exotoxin A
 PT - able to cross membranes and deliver to the cytoplasm, e.g. nucleic
 PT acids, antibodies, tumour suppressors etc.
 XX
 PS Disclosure; Page 8; 76pp; English.
 XX
 CC This peptide is located at the C-terminal end of exotoxin A (ETA, see
 CC AAW76391) of Pseudomonas aeruginosa. The motif is important in the
 CC intracellular transport and cytotoxicity of ETA. Loss of REDL inhibits
 CC the ability of ETA to reach the cytoplasm. However, REDL can be
 CC substituted by KDEL (see AAW76396) without loss of cytotoxicity. The
 CC invention provides a means of delivering compounds to cells as conjugates
 CC with modified ETA. The modified ETA is able to cross membranes and
 CC deliver e.g. therapeutic agents to the cytoplasm, such as nucleic acids,
 CC peptides, peptide nucleic acids, single chain antibodies and tumour
 CC suppressors
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db ||||
 1 REDL 4
 RESULT 3
 AAW52263
 ID AAW52263 standard; peptide; 4 AA.
 XX
 AC AAW52263;
 XX
 DT 18-JUN-1998 (first entry)
 XX
 DE C-terminal fragment of pseudomonas exotoxin.
 XX
 KW Pseudomonas exotoxin; PE; cytotoxic.
 XX
 OS Pseudomonas sp.
 XX
 PN US5705163-A.
 XX
 PD 06-JAN-1998.
 XX
 PF 05-JUN-1995; 95US-00461233.
 XX
 PR 02-JAN-1990; 90US-00459635.
 PR 12-MAY-1990; 90US-00522563.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Fitzgerald D, Pastan I, Chaudhary VK;
 XX
 DR WPI; 1998-086092/08.
 XX
 XX Methods for killing target cells - with recombinant Pseudomonas exotoxin
 PT fusion proteins.
 XX
 PS Claim 8; Col 14; 12pp; English.

XX This sequence represents a C-terminal fragment of a Pseudomonas exotoxin
 CC (PE). This sequence can be used in the method of the invention for
 CC killing a target cell, which comprises contacting the cell with a
 CC recombinant Pseudomonas exotoxin (PE) having: (a) a recognition molecule
 CC that binds to the target cell and is inserted in domain III after amino
 CC acid 600 and before amino acid 613 of the PE, and (b) a carboxy-terminal
 CC sequence of 4-16 amino acids that permits translocation of the PE into
 CC the cytosol of the target cell. The insertion of a recognition molecule
 CC allows selective killing of target cells without significant cytotoxicity
 CC to other cells not recognised
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db ||||
 1 REDL 4
 RESULT 4
 ABB76202
 ID ABB76202 standard; peptide; 4 AA.
 XX
 AC ABB76202;
 XX
 DT 05-AUG-2002 (first entry)
 XX
 DE Peptide used to modify Pseudomonas exotoxin.
 XX
 KW Exotoxin; Pseudomonas; immunotoxin; mesothelin; scFv; mesothelioma;
 KW ovarian cancer; stomach cancer; squamous cell cancer; antitumour;
 KW therapy; diagnosis.
 XX
 OS Synthetic.
 XX
 PN WO9928471-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 25-NOV-1998; 98WO-US025270.
 XX
 PR 01-DEC-1997; 97US-0067175P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Pastan IH, Chowdhury PS;
 XX
 DR WPI; 1999-371123/31.
 XX
 PT New anti-mesothelin antibodies.
 XX
 PS Disclosure; Page 29; 63pp; English.
 XX
 CC The present sequence is a peptide that can be added to the C-terminal end
 CC of a Pseudomonas exotoxin (PE) to produce a modified PE. Claimed
 CC immunoconjugates comprise a therapeutic agent, such as PE or a cytotoxic
 CC fragment of PE, and an anti-mesothelin antibody, such as scFv SS (see
 CC ABB76197), and are obtained by recombinant methods. The recombinant
 CC immunoconjugates are used in a claimed method for inhibiting the growth
 CC of a malignant cell that expresses mesothelin on its cell surface,
 CC especially in mesothelioma, ovarian cancer, stomach cancer or squamous
 CC cell cancer
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
1111
Db 1 REDL 4

RESULT 6
AAW92910
ID AAW92910 standard; protein; 4 AA.
XX AAW92910;
AC AAW92910;
XX 17-MAY-1999 (first entry)
DT Pseudomonas sp. exotoxin A PE ER retention peptide motif #2.
DE Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;
XX antibody production; non-native epitope; immune response; antigen;
KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;
KW secretory; IGA-mediated; mucosal surface; IGA antibody; retention domain;
KW endoplasmic reticulum.
XX Pseudomonas sp.
OS Pseudomonas sp.
PN WO9902712-A1.
XX WO9902712-A1.
XX 21-JAN-1999.
PD 21-JAN-1999.
XX 10-JUL-1998; 98WO-US014336.
PF 10-JUL-1998; 98WO-US014336.
XX 11-JUL-1997; 97US-0056924P.
PR 11-JUL-1997; 97US-0056924P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GETH) GENENTECH INC.
XX Fitzgerald DJ, Mreny RJ;
PI WPI; 1999-120913/10.
XX WPI; 1999-120913/10.
XX New Pseudomonas exotoxin chimeric immunogens - comprise a foreign epitope
PT for producing an immune response to pathogens, e.g. virus, bacteria or
PT protozoa or to cancer antigens.
XX Disclosure; Page 33; 85pp; English.

PS The present invention describes a method in which a secretory IGA-mediated
XX immune response is elicited in a subject. The method involves
CC administering to at least 1 mucosal surface of the subject a non-toxic
CC Pseudomonas exotoxin A-like (PE-like) chimeric immunogen comprising a
CC cell recognition domain of that binds to a cell surface receptor on the
CC mucosal surface, a translocation domain comprising an amino acid sequence
CC of PE domain II to effect translocation to a cell cytosol, a foreign
CC epitope domain comprising an amino acid sequence of that encodes a
CC foreign epitope, and a sequence encoding an endoplasmic reticulum (ER)
CC retention domain that comprises an ER retention sequence. Also described
CC is a composition comprising secretory IGA antibodies that specifically
CC recognise an epitope of HIV-1. The method can be used for eliciting an
CC immune response to pathogens, e.g. virus, bacteria or parasitic protozoa
CC or to a cancer antigen. The antibodies produced can also be isolated and
CC used, e.g. for affinity chromatography. The PE immunogens can be made by
CC wholly recombinant techniques which allows insertion of existing variants
CC of an epitope, or new variants of rapidly evolving epitopes. The PE can
CC be engineered to alter the function of its domains, thereby providing a
CC variety of activities, e.g. by replacing the native cell binding domain
CC of PE A (domain Ia) with a ligand for a particular cell type. By providing
CC a cell recognition domain that binds to a mucosal surface a secretory
CC immune response involving IGA can be elicited. This sequence represents a
CC PE protein endoplasmic reticulum (ER) retention domain motif
XX Sequence 4 AA;
SQ Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
1111
Db 1 REDL 4

RESULT 5
AAW92910
ID AAW92910 standard; protein; 4 AA.
XX AAW92910;
AC AAW92910;
XX 17-MAY-1999 (first entry)
DT Pseudomonas sp. exotoxin A PE ER retention peptide motif #2.
DE Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;
XX antibody production; non-native epitope; immune response; antigen;
KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;
KW secretory; IGA-mediated; mucosal surface; IGA antibody; retention domain;
KW endoplasmic reticulum.
XX Pseudomonas sp.
OS Pseudomonas sp.
PN WO9902712-A1.
XX WO9902712-A1.
XX 21-JAN-1999.
PD 21-JAN-1999.
XX 10-JUL-1998; 98WO-US014336.
PF 10-JUL-1998; 98WO-US014336.
XX 11-JUL-1997; 97US-0056924P.
PR 11-JUL-1997; 97US-0056924P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GETH) GENENTECH INC.
XX Fitzgerald DJ, Mreny RJ;
PI WPI; 1999-120913/10.
XX WPI; 1999-120913/10.
XX New Pseudomonas exotoxin chimeric immunogens - comprise a foreign epitope
PT for producing an immune response to pathogens, e.g. virus, bacteria or
PT protozoa or to cancer antigens.
XX Disclosure; Page 33; 85pp; English.

Db 1 REDL 4

RESULT 7
AAW92924
ID AAW92924 standard; protein; 4 AA.
AC AAW92924;
XX
XX
DT 17-MAY-1999 (first entry)
XX
XX Pseudomonas sp. exotoxin A PE ER retention peptide motif #2.
DE
XX
KW Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;
KW antibody production; non-native epitope; immune response; antigen;
KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;
KW secretory; ER; endoplasmic reticulum; retention sequence.
XX
OS Pseudomonas sp.
XX
XX WO9902713-A1.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US014341.
XX
XX 11-JUL-1997; 97US-0052375P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fitzgerald DJ;
XX
XX WPI; 1999-120914/10.
XX
XX New Pseudomonas exotoxin chimeric immunogens - comprise a non-native
PT epitope for producing an immune response to pathogens, e.g. virus,
PT bacteria, or protozoa or to cancer antigens.
XX
XX Claim 13; Page 64; 92pp; English.
XX
XX This invention describes a non-toxic Pseudomonas exotoxin A-like (PE-
CC like) chimeric immunogen. This PE-like immunogen can be used in vaccines
CC and for producing antibodies against the non-native epitope. It can be
CC used for producing an immune response to a pathogen, e.g. a virus,
CC bacteria or parasitic protozoa or a cancer antigen. The antibodies can
CC also be isolated and used for e.g. affinity chromatography. The PE
CC immunogens can be made by wholly recombinant techniques which allows
CC insertion of existing variants of an epitope, or new variants of rapidly
CC evolving epitopes. The PE can be engineered to alter the function of its
CC domains, thereby providing a variety of activities, e.g. by replacing the
CC native cell binding domain of PE A (domain Ia) with a ligand for a
CC particular cell receptor, the chimera can be targeted to bind to the
CC and secretory immune responses against the non-native epitope. This
CC sequence represents a PE protein endoplasmic reticulum (ER) retention
CC domain motif
XX
XX Sequence 4 AA;
SQ

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDL 4
DB 1 REDL 4

RESULT 8
AAB49323
ID AAB49323 standard; protein; 4 AA.
XX
XX AAB49323;
AC

XX 01-MAR-2001 (first entry)
DT
XX Endosomal escape motif.
DE
XX Permeation enhancer; nucleic-acid based drug; caprylic acid;
KW intracellular delivery; capric acid.
KW
XX Unidentified.
OS
XX WO200067798-A2.
PN
XX 16-NOV-2000.
PD
XX 05-MAY-2000; 2000WO-GB001726.
XX
XX 05-MAY-1999; 99US-0132603P.
PR
XX (ELAN-) ELAN CORP PLC.
PA (DENI/) DENISON C M.
XX
XX Seveso M, O'mahony DJ, Page DT;
PI
XX WPI; 2001-049723/06.
XX
XX Method for enhancing the intracellular delivery of a nucleic acid-based
PT drug comprises administering in combination with an enhancer.
PT
XX Disclosure; Page 8; 42pp; English.
PS
XX The present invention provides novel methods of enhancing the
CC intracellular delivery of nucleic-acid based drugs. These involve the use
CC of formulations containing not only the nucleic acid of interest, but
CC also a permeation enhancer such as caprylic acid or capric acid. This is
CC particularly useful for the delivery of drugs into the cells of the
CC gastrointestinal tract, especially the small intestine
XX
XX Sequence 4 AA;
SQ

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDL 4
DB 1 REDL 4

RESULT 9
AAU96732
ID AAU96732 standard; peptide; 4 AA.
XX
XX AAU96732;
AC
XX 30-JUL-2002 (first entry)
DT
XX Human XAGE-1 p9 and XAGE-1 p16 associated C-terminal peptide #2.
DE
XX XAGE-1; p9; p16; major histocompatibility complex; T lymphocyte; cancer;
KW prostate cancer; lung cancer; small cell carcinoma;
KW non-small cell carcinoma; squamous cell carcinoma; adenocarcinoma;
KW ovarian cancer; breast cancer; glioblastoma; pancreatic cancer;
KW T cell lymphoma; melanoma; histocytic lymphoma; Ewing's sarcoma;
KW rhabdomyosarcoma; osteosarcoma.
XX
XX Unidentified.
OS
XX WO200218584-A2.
PN
XX 07-MAR-2002.
PD
XX 31-AUG-2001; 2001WO-US027258.
XX
XX

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PR 01-SEP-2000; 2000US-0229684P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pastan IH, Liu XF, Bera TK, Lee B, Eglund KA;
XX
XX WPI; 2002-382965/41.
XX
XX Polypeptide from xage-1 p9 or pl6 protein, which is expressed by a gene
XX expressed in multiple cancers useful for activating T lymphocytes against
XX cells expressing the protein.
XX
XX Disclosure; Page 44; 79pp; English.
XX
XX The invention describes an isolated polypeptide (I) comprising xage-1 p9
XX or pl6 protein (p9p/pl6p) which, when processed and presented in context
XX of major histocompatibility complex molecules, activates T lymphocytes
XX against cells which express p9p/pl6p. (I), a vector encoding the protein
XX (II) or a composition containing (I) is useful for the manufacture of a
XX medicament for treatment of cancer e.g. of the prostate, lung (especially
XX lung cancer from small cell carcinoma, non-small cell carcinoma, squamous
XX cell carcinoma, and adenocarcinoma), ovarian, breast, glioblastoma,
XX pancreatic, T cell lymphoma, melanoma, and histocytic lymphoma; or
XX Ewing's sarcoma, rhabdomyosarcoma and osteosarcoma. The method involves
XX administering (II) in a recombinant virus, or immunising the subject with
XX an expression vector that expresses polypeptide comprising an epitope of
XX p9p and which is an autologous recombinant cell. The method is useful for
XX inhibiting the growth of a cancer cell expressing p9p on its exterior
XX surface. (II) is useful for determining if a subject has an p9p
XX expressing cancer by taking a cell sample from the subject from a site
XX other than the testes, and determining if a cell in the sample contains a
XX nucleic acid transcript encoding p9p, or detecting p9p produced by
XX transfection of the transcript, where the method preferably comprises
XX contacting RNA from the cell with a nucleic acid probe that specifically
XX hybridises to the transcript under hybridisation conditions and detecting
XX hybridisation, or comprises disrupting the cell preferably a lymph node
XX and contacting a portion of the cell contents with a chimeric molecule
XX comprising a targeting moiety and a detectable label, where the targeting
XX moiety specifically binds to p9p and detecting the label bound to p9p.
XX This sequence represents a peptide that can be added to the C-terminal of
XX the human membrane associated XAGE-1 pl6 protein or intracellular XAGE-1
XX p9 protein in order to study protein expression
XX
XX Sequence 4 AA;
XX
XX Query Match 100.0%; Score 20; DB 5; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 REDL 4
XX |||||
XX Db 1 REDL 4
XX
XX RESULT 10
XX AAE28524
XX ID AAE28524 standard; peptide; 4 AA.
XX
XX AC AAE28524;
XX
XX DT 27-DEC-2002 (first entry)
XX
XX DE Endoplasmic reticulum (ER) retention peptide #2.
XX
XX Pseudomonas exotoxin A; PE; type IV pilin loop; immune response;
XX infection; gene therapy; antimicrobial; endoplasmic reticulum; ER;
XX immunostimulant.
XX
XX OS Unidentified.
XX
XX PN WO200260935-A2.
XX
XX DB 08-AUG-2002.
XX

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XX 20-DEC-2001; 2001WO-US049143.
XX
XX 21-DEC-2000; 2000US-0257877P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fitzgerald D;
XX
XX WPI; 2002-698546/75.
XX
XX New chimeric proteins comprising a non-toxic Pseudomonas exotoxin A
XX sequence and a Type IV pilin loop sequence, useful for preventing and
XX treating infections of microorganisms, e.g. Pseudomonas aeruginosa,
XX Neisseria meningitidis.
XX
XX Disclosure; Page 66; 89pp; English.
XX
XX The invention relates to chimeric proteins comprising a non-toxic
XX Pseudomonas exotoxin A (PE) and a Type IV pilin loop. The chimeric
XX proteins are useful for eliciting an immune response in a host. They are
XX also useful for preventing and treating infections of microorganisms,
XX e.g. Pseudomonas aeruginosa, Neisseria meningitidis, Neisseria
XX gonorrhoeae, Vibrio cholera, Pasteurella multocida or Candida. The
XX chimeric proteins and compositions are useful for diagnostic tests such
XX as immunoassays, to detect the presence of microorganisms bearing a Type
XX IV pilin loop sequence, or to determine whether a host has antisera
XX against a Type IV pilin loop due to an infection. They can also be used
XX to purify antibodies against the Type IV pilin loop sequence. The
XX invention is also used in gene therapy. The present sequence is
XX endoplasmic reticulum (ER) retention peptide used in the invention
XX
XX Sequence 4 AA;
XX
XX Query Match 100.0%; Score 20; DB 5; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 REDL 4
XX |||||
XX Db 1 REDL 4
XX
XX RESULT 11
XX AAE33356
XX ID AAE33356 standard; peptide; 4 AA.
XX
XX AC AAE33356;
XX
XX DT 02-APR-2003 (first entry)
XX
XX DE Endoplasmic retention peptide #2.
XX
XX MUC-1; 3D; variable light domain; VL; variable heavy domain; VH; diabody;
XX cancer; antibody; therapy.
XX
XX OS Unidentified.
XX
XX PN WO200279429-A2.
XX
XX PD 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009735.
XX
XX 30-MAR-2001; 2001US-0280721P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Denardo SJ, Winthrop MD, Denardo GL;
XX
XX WPI; 2003-046804/04.
XX
XX Novel antibody that specifically binds to cancer antigen MUC-1 useful for
XX

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PT detecting a cell bearing MUC-1 antigen, comprises variable light or
 XX variable heavy domains of antibodies 12E, 3D, A5 or C4.
 PS Disclosure; Page 23; 75pp; English.
 XX
 CC The invention relates to a novel antibody that specifically binds to the
 CC cancer antigen MUC-1. The antibody comprises a domain having a sequence
 CC of a polypeptide selected from 12E variable light (VL) or variable heavy
 CC (VH) domain, 3D VL or VH domain, A5 VL or VH domain and C4 VL or VH
 CC domain. Antibodies of the invention are useful for detecting a cell
 CC bearing a MUC-1 antigen. The invention is useful for producing a variety
 CC of human or humanised antibodies or diabodies. The invention is also
 CC useful for treating cancer. The present sequence is endoplasmic retention
 CC peptide, used in the invention
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 1 REDL 4
 RESULT 12
 ABR61856
 ID ABR61856 standard; peptide; 4 AA.
 XX
 AC ABR61856;
 XX
 DT 12-SEP-2003 (first entry)
 XX
 DE Pseudomonas exotoxin carboxy terminal fragment.
 XX
 KW Interleukin; IL-13; antiallergic; antiasthmatic; respiratory; PE;
 KW antiinflammatory; tuberculostatic; antimicrobial; antibacterial;
 KW antiparasitic; virucide; fungicide; exotoxin.
 XX
 OS Pseudomonas sp.
 XX
 FN WO2003047632-A1.
 XX
 PD 12-JUN-2003.
 XX
 PF 28-FEB-2002; 2002WO-IB000616.
 XX
 PR 04-DEC-2001; 2001US-0337179P.
 XX
 PA (UNMI) UNIV MICHIGAN.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Puri RK, Hogaboam CM, Jakubzick C, Kunkel SL;
 XX
 DR WPI; 2003-523269/49.
 XX
 XX Use of chimeric molecule comprising a toxic moiety and a targeting moiety
 PT binding to interleukin-13 receptor or a nucleic acid sequence encoding
 PT the molecule in the treatment of e.g. allergy and asthma.
 XX
 PS Disclosure; Page 34; 105pp; English.
 XX
 CC The invention provides a chimeric molecule comprising a toxic moiety and
 CC a targeting moiety or a nucleic acid sequence encoding the chimeric
 CC molecule, for use in the manufacture of a medicament. The targeting
 CC moiety binds specifically to a cell surface receptor for interleukin-13
 CC (IL-13). The molecule can be used for application to a respiratory tract
 CC of a mammal to alleviate symptoms of a TH-2-type cytokine mediated
 CC disorders e.g. allergy, asthma, excess mucus production, airway
 CC inflammation, airway hyper responsiveness, tuberculosis, formation of
 CC granulomas during tuberculosis; and respiratory tract symptoms of viral,
 CC bacterial, fungal and parasitic infections (e.g. leishmania, filariasis

CC and schistosomiasis). Sequences ABR61855-56 represent pseudomonas
 CC exotoxin carboxy terminal fragments
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 1 REDL 4
 RESULT 13
 ADC84561
 ID ADC84561 standard; peptide; 4 AA.
 XX
 AC ADC84561;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Carboxyl terminus peptide sequence of the invention #2.
 XX
 KW anti-CD22 antibody; RFB4; Cytostatic; Gene therapy; CD22-Antagonist;
 KW cancer.
 XX
 OS Unidentified.
 XX
 FN WO2003027135-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 25-SEP-2002; 2002WO-US030316.
 XX
 PR 26-SEP-2001; 2001US-0325360P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Pastan IH, Salvatore G, Beers R, Kreitman RJ;
 XX
 DR WPI; 2003-402972/38.
 XX
 XX New anti-CD22 antibody, useful for the manufacture of a medicament for
 PT detecting or inhibiting growth of CD22+ cancer cell, comprising variable
 PT heavy and light chains of RFB4 antibody.
 XX
 PS Disclosure; SEQ ID NO 6; 59pp; English.
 XX
 CC The present invention relates to a new anti-CD22 antibody has variable
 CC light (VL) and variable heavy (VH) chains of the antibody RFB4. The anti-
 CC CD22 antibody is useful for the manufacture of a medicament for detecting
 CC or inhibiting growth of CD22+ cancer cell. The present sequence
 CC represents a carboxyl terminus sequence of the invention.
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 1 REDL 4
 RESULT 14
 ADG25841
 ID ADG25841 standard; peptide; 4 AA.
 XX
 AC ADG25841;
 XX
 DT 11-MAR-2004 (first entry)

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XX Pseudomonas exotoxin (PE) related peptide SEQ ID NO:31.
DE antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer.
XX Synthetic.
OS Pseudomonas sp.
XX WO2003104432-A2.
PN 18-DEC-2003.
XX 09-JUN-2003; 2003WO-US018373.
XX 07-JUN-2002; 2002US-0387293P.
PR 16-SEP-2002; 2002US-0411032P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Pastan IH, Nagata S, Onda M, Numata Y, Santora K, Beers R;
PI Kreitman R, Sinha A;
XX WPI; 2004-062352/06.
XX New antibody that binds specifically to a stalk of CD30 of a cell, or to
PT an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact
PT CD30, useful for inhibiting the growth of a CD30+ cancer cell.
XX Disclosure; SEQ ID NO 31; 102pp; English.
XX The present invention describes an isolated antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of soluble CD30 (sCD30) from intact CD30. Also described:
CC (1) a composition comprising the antibody conjugated or fused to a
CC therapeutic part; (2) a nucleic acid encoding an antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of sCD30 from intact CD30; (3) an expression vector
CC comprising the nucleic acid operably linked to a promoter; (4) inhibiting
CC growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell
CC in a biological sample; (6) a host cell expressing the isolated nucleic
CC acid encoding the antibody having variable heavy and variable light
CC chains; and (7) a kit for detecting the presence of a CD30+ cancer cell
CC in a biological sample comprising a container and an anti-CD30 antibody.
CC An anti-CD30 antibody has cytostatic activity, and can be used in gene
CC therapy. The anti-CD30 antibody that binds specifically to a stalk of
CC CD30 of a cell, or to an epitope destroyed upon cleavage of sCD30 from
CC intact CD30 is useful for the manufacture of a medicament for inhibiting
CC the growth of a CD30+ cancer cell. The present sequence is used in the
CC exemplification of the present invention.
XX Sequence 4 AA;
SQ Query Match 100.0%; Score 20; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDL 4
Db ||||
1 REDL 4
RESULT 15
ADN07007
ID ADN07007 standard; peptide; 4 AA.
XX AC ADN07007;
XX 01-JUL-2004 (first entry)
XX Pseudomonas aeruginosa translocation signalling peptide #2.
DE Bispecific single chain; bs-scFv; cancer;
XX epidermal growth factor receptor; EGFR; therapy;
KW

KW translocation signalling peptide.
XX Pseudomonas aeruginosa.
XX US2004071696-A1.
PN 15-APR-2004.
XX 04-APR-2003; 2003US-00406830.
PF 05-APR-2002; 2002US-0370276P.
PR (REGC) UNIV CALIFORNIA.
XX (FOXC-) FOX CHASE CANCER CENT.
PA Adams GP, Horak EM, Weiner LM, Marks JD;
XX WPI; 2004-328525/30.
XX Novel bispecific antibody comprising first and second antibody joined to
PT each other and having binding specificity to different epitopes of
PT Epidermal Growth Factor Receptor protein, useful for treating cancer.
XX Disclosure; SEQ ID NO 24; 57pp; English.
XX The present invention provides bispecific single chain (bs-scFv) antibody
CC molecules which may be used to treat various forms of cancer associated
CC with the overexpression of the epidermal growth factor receptor (EGFR)
CC family. The invention is useful for specifically delivering an effector
CC molecule to a cell bearing a receptor from EGFR protein family chosen
CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the
CC treatment of cancer. The present sequence is Pseudomonas aeruginosa
CC translocation signalling peptide. The peptide is used in the invention.
XX Sequence 4 AA;
SQ Query Match 100.0%; Score 20; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDL 4
Db ||||
1 REDL 4
RESULT 16
ADP64378
ID ADP64378 standard; peptide; 4 AA.
XX AC ADP64378;
XX 09-SEP-2004 (first entry)
XX Carboxyl terminus peptide SEQ ID NO:6.
DE human; breast cancer and salivary gland expression protein; BASE;
XX cytostatic; immunostimulant; gene therapy;
KW radioimmunotherapeutic targeted therapy; breast cancer.
XX Synthetic.
OS WO2004053098-A2.
XX 24-JUN-2004.
PD 10-DEC-2003; 2003WO-US039476.
XX 10-DEC-2002; 2002US-0432531P.
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Pastan IH, Egland KA, Vincent JJ, Lee B, Strausberg R;
XX

DR WPI; 2004-480931/45.
 XX New breast cancer associated gene, termed BASE (breast cancer and
 PT salivary gland expression), and the encoded polypeptide and associated
 PT reagents, useful in diagnosis and treatment of breast cancer.
 XX
 XX Disclosure; SEQ ID NO 6; 86pp; English.
 XX
 CC The present invention describes an isolated polypeptide (I) comprising an
 CC amino acid sequence selected from human breast cancer and salivary gland
 CC expression (BASE) proteins BASE1 and BASE2 (SEQ ID Nos:1 and 2), and
 CC their fragments and variants, which when processed and presented in the
 CC context of major histocompatibility complex (MHC) molecules, activates T
 CC lymphocytes against cells which express BASE1 or BASE2 (SEQ ID Nos:1 or
 CC 2). The human BASE gene is located on chromosome 20. (I) has cytostatic
 CC and immunostimulant activities, and can be used in gene therapy, and in
 CC radioimmunotherapeutic targeted therapy using antibodies against BASE
 CC polypeptides. The BASE polypeptides, nucleic acids, antibodies and
 CC compositions of the present invention can be used for the diagnosis and
 CC treatment of breast cancer. The present sequence represents a carboxyl
 CC terminus peptide, which is given in the exemplification of the present
 CC invention.
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 20; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 1 REDL 4
 RESULT 17
 ADP79648
 ID ADP79648 standard; peptide; 4 AA.
 XX
 AC ADP79648;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Pseudomonas exotoxin A C-terminal extension #2.
 XX
 XX heavy chain; variable region; VH; VL; 8H9; scFv; monoclonal antibody;
 KW antigen; light chain; effector molecule; toxin; epitope; Pseudomonas;
 KW exotoxin; PE38; PE40; PE38KDEL; PE38REDL; tumour; breast cancer;
 KW glioblastoma; glioma; astrocytoma; synovial sarcoma.
 XX
 OS Synthetic.
 XX
 XX WO2004050849-A2.
 PN
 XX 17-JUN-2004.
 PD
 PF 01-DEC-2003; 2003WO-US038227.
 XX
 XX 02-DEC-2002; 2002US-0430305P.
 PR
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Pastan I, Onda M, Cheung N;
 PI
 XX WPI; 2004-461118/43.
 DR
 XX New isolated Fv protein comprises a variable region of a heavy chain and
 PT light chain of a monoclonal antibody that binds the antigen specifically
 PT bound by monoclonal antibody 8H9, useful for treating tumors, e.g.
 PT astrocytoma or glioblastoma.
 XX
 XX Disclosure; Page 32; 79pp; English.
 PS
 XX

CC This sequence represents a possible C-terminal extension of a native
 CC pseudomonas exotoxin (PE) A. PE-A has a molecular weight of 66 kD. It
 CC acts to inhibit protein synthesis in eukaryotic cells by inactivating the
 CC ADP-ribosylation of elongation factor-2. This protein was used in the
 CC production of an Fv protein comprising a variable region of a heavy chain
 CC of a monoclonal antibody that binds the antigen specifically bound by
 CC monoclonal antibody 8H9 and a variable region of a light chain of the
 CC monoclonal antibody that binds the antigen specifically bound by
 CC monoclonal antibody 8H9, and an effector molecule comprising a toxin,
 CC where the Fv protein specifically binds the epitope bound by monoclonal
 CC antibody 8H9. The toxin is preferably a Pseudomonas exotoxin, selected
 CC from PE38, PE40, PE38KDEL, or PE38REDL. The Fv protein comprising a Fv
 CC polypeptide comprising both the light and the heavy chains of an antibody
 CC that binds the antigen specifically bound by 8H9 and an effector molecule
 CC comprising a toxin covalently linked to the Fv polypeptide is useful for
 CC the manufacture of a medicament for the treatment of a tumour. The tumour
 CC includes breast cancer, a glioblastoma, a mixed glioma, an astrocytoma,
 CC or a synovial sarcoma.
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 20; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 1 REDL 4
 RESULT 18
 ADZ21546
 ID ADZ21546 standard; peptide; 4 AA.
 XX
 AC ADZ21546;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Endoplasmic reticulum retention peptide.
 XX
 KW Single chain antibody; MUC-1; tumor-associated antigen; antibody therapy;
 KW cytostatic.
 XX
 OS Synthetic.
 XX
 XX WO2005032454-A2.
 PN
 XX 14-APR-2005.
 PD
 PF 07-MAY-2004; 2004WO-US014159.
 XX
 XX 09-MAY-2003; 2003US-00435614.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Denardo SJ, Winthrop MD, Denardo GL, Xiong C;
 PI
 XX WPI; 2005-285319/29.
 DR
 XX New antibodies that specifically bind to cancer antigen MUC-1, useful for
 PT tumor targeting, for inhibiting the growth or proliferation of cancer
 PT cells or as diagnostic agents to identify tumors and monitor levels of
 PT circulating antigen.
 XX
 XX Disclosure; SEQ ID NO 12; 79pp; English.
 PS
 XX The invention provides novel antibodies that specifically bind to the MUC
 CC -1 cancer antigen. Preferred single chain antibodies were obtained from a
 CC phage display library and were designated as 12E, 3D, A5, C4, B5, E1 and
 CC B9 ADZ21537-ADZ21543. The heavy chain variable regions (VH) and light
 CC chain variable regions (VL) of these antibodies are also provided
 CC ADZ21523-ADZ21536. The VH and VL domains govern the specificity and
 CC binding affinity of the antibodies and permit the construction of a

CC variety of antibodies that specifically target the MUC-1 antigen and
CC cells bearing/displaying the antigen. The antibodies are useful targeting
CC moieties for specifically directing imaging agents and various
CC therapeutic moieties to a cancer. A claimed method of inhibiting the
CC growth or proliferation of a cell bearing a MUC-1 antigen comprises
CC contacting the cell with a chimeric molecule comprising an anti-MUC-1
CC antibody attached to a cytotoxin, a radionuclide, a liposome comprising
CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present
CC sequence is that of an endoplasmic reticulum retention peptide that can
CC be added to the Pseudomonas exotoxin A (PE) moiety of chimeric molecules
CC of the invention. Note: this sequence is referred to as SEQ ID NO:12 on
CC page 24 of the specification, but differs from the sequence given as SEQ
CC ID NO:12 on page 16 ADZ21534.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|
|
|
|
Db 1 REDL 4

RESULT 19
AEA50149
ID AEA50149 standard; peptide; 4 AA.

AC AEA50149;

DT 11-AUG-2005 (first entry)

XX Pseudomonas endotoxin cytosolic translocation sequence #2.

XX Cytostatic; Antibody therapy; complementarity determining region; CDR;
KW CD22; Pseudomonas exotoxin; PE; antibody; cancer.

XX Homo sapiens.

OS Synthetic.

PN WO2005052006-A2.

XX 09-JUN-2005.

XX 24-NOV-2004; 2004WO-US039617.

XX 25-NOV-2003; 2003US-0525371P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Paetan IH, Ho M, Bang S;

XX WPI; 2005-405363/41.

XX New antibody that specifically binds CD22, useful for the manufacture of
PT a medicament to inhibit the growth of a CD22+ cancer cell, thus useful
PT for treating cancer.

XX Disclosure; SEQ ID NO 6; 106pp; English.

XX This sequence represents a fragment of Pseudomonas endotoxin (PE) which
CC maintains the ability of the construct to translocate into the cytosol.
CC The PE was used in conjunction with the antibody of the invention which
CC specifically binds CD22. The antibody of the invention may be used in the
CC generation of a chimeric molecule, which may also comprise a therapeutic
CC moiety. The therapeutic moiety is preferably a Pseudomonas exotoxin (PE)
CC A or its cytotoxic fragment or mutant, where the PE has a Gly, Ala, Val,
CC Leu or Ile in place of Arg at position 490 of the 613 amino acids wild
CC type PE sequence. The antibody and chimeric molecule are useful for the
CC manufacture of a medicament to inhibit the growth of a CD22+ cancer cell,
CC and thus are useful for treating cancer.

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|
|
|
|
Db 1 REDL 4

RESULT 20
AEB27747
ID AEB27747 standard; peptide; 4 AA.

XX AEB27747;

XX 22-SEP-2005 (first entry)

XX Anti-prostate cancer-antibody related translocation peptide SEQ ID NO 19.
DE
KW cytostatic; antibody therapy; pharmaceutical; cancer; metastasis;
KW solid tumor; prostate tumor; neoplasm.

OS Synthetic.

XX WO2005062977-A2.

XX 14-JUL-2005.

XX 21-DEC-2004; 2004WO-US043574.

XX 23-DEC-2003; 2003US-0532433P.

XX (REGC) UNIV CALIFORNIA.

XX Liu B, Marks JD;

XX WPI; 2005-522452/53.

XX Novel antibody that specifically binds and is internalized into prostate
PT cancer cell, useful for inhibiting growth or proliferation of prostate
PT cancer cell and for detecting prostate cancer cell.

XX Disclosure; SEQ ID NO 19; 77pp; English.

XX The invention describes an antibody (I) that specifically binds and is
CC internalized into a prostate cancer cell, comprising an antibody that
CC specifically binds an epitope that is specifically bound by an antibody
CC chosen from A33 (SEQ ID No. 22), M10A12 (SEQ ID No. 23), M9P4 (SEQ ID No.
CC 24), OA12 (SEQ ID No. 25), M1G12 (SEQ ID No. 26), M1F12 (SEQ ID No.
CC 27), and C10 (SEQ ID No. 28). Also described are: a chimeric molecule
CC (II), comprising an effector attached to (I); a pharmaceutical
CC formulation (III) comprising an excipient and (I) or (II); detecting (M1)
CC a prostate cancer cell, comprising contacting the prostate cancer cell
CC with (II) attached to an epitope tag, contacting (II) with a chelate
CC comprising a detectable group, where the chelate binds to the epitope tag
CC therefore associating the detectable group with the chelate and detecting
CC the detectable group; a nucleic acid (IV) comprising a nucleic acid that
CC encodes (I); an expression vector (V) comprising (IV); a cell comprising
CC (V); and a kit (VI) comprising a container containing (I), (I) and a
CC chimeric molecule (II) are useful for inhibiting the growth or
CC proliferation of a prostate cancer cell, which involves contacting the
CC cell with (I), or with (II) attached to a cytotoxin or radionuclide. The
CC cell is a metastatic cell or solid tumor cell. (II) is useful for
CC detecting a prostate cancer cell, which involves contacting the prostate
CC cancer cell with (II) attached to a detectable label and detecting the
CC presence or absence of the detectable label. This is the amino acid
CC sequence of a cell membrane translocation peptide used in the creation of
CC single chain anti-prostate cancer-antibodies.

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 1 REDL 4

RESULT 21
 AEB31417
 ID AEB31417 standard; peptide; 4 AA.

XX AC AEB31417;

XX XX 22-SEP-2005 (first entry)

XX DE Endoplasmic reticulum localization signal #16.

XX KW screening; antibody; caspase; apoptosis; cell proliferation; cancer;
 KW transfection; autoimmune disease; inflammation; infectious disease;
 KW cytostatic; immunosuppressive; anti-inflammatory; antimicrobial;
 KW endoplasmic reticulum; ER; protein localization; antibody engineering.

XX OS Unidentified.

XX XX WO2005063817-A2.

XX XX 14-JUL-2005.

XX XX 21-DEC-2004; 2004WO-US042937.

XX XX 22-DEC-2003; 2003US-0531714P.

XX PR 31-DEC-2004; 2004US-0605902P.

XX XX (AMGE-) AMGEN INC.

XX PI Yan W, Shen W, Zhou H, Zhou C, Cosman DJ, Carter P, Martin FH;
 XX WPI; 2005-497894/50.

XX PT Enriching for nucleic acids encoding functional antibodies, useful for
 PT treating cancer, autoimmune, inflammatory and infectious diseases, by
 PT transfecting cells with polynucleotides encoding multimeric antibodies
 and a vector.

XX PS Disclosure; Page 16; 93pp; English.

XX CC This invention describes a novel method of screening for nucleic acids
 CC encoding multimeric antibodies having a biological function e.g. caspase
 CC activity, apoptosis, and/or inhibition of proliferation of cancer cells.
 CC The invention also describes 1) a method for identifying mammalian
 CC transfectants expressing scFv-Fcs on their cell surfaces; 2) a method for
 CC enriching for variant proteins that bind to a molecule with different
 CC affinity than the original and 3) a group of mammalian cells displaying a
 CC group of at least 100 different recombinant human antibodies on their
 CC cell surfaces, where a library of nucleic acids encoding the group of
 CC antibodies has been introduced into the cells via transfection using a
 CC vector that does not comprise sequences derived from vaccinia virus or a
 CC group of mammalian cells transfected with nucleic acids encoding at least
 CC 100 different scFv-Fcs, where the transfected cells express at least 100
 CC different scFv-Fcs on their cell surfaces. The products of the invention
 CC can be used for treating cancer, autoimmune, inflammatory and infectious
 CC diseases. This sequence represents an endoplasmic reticulum localization
 CC sequence which can direct a protein to be retained within a cell.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4

Db 1 REDL 4
 ||||

RESULT 22

AAR95064
 ID AAR95064 standard; peptide; 5 AA.

XX AC AAR95064;

XX DT 18-AUG-1996 (first entry)

XX DE Pseudomonas exotoxin endoplasmic reticulum retention signal.

XX KW Nucleic acid transfer system; Gene transfer; gene therapy;

XX KW cell targeting; multidomain protein; vector; cancer;

XX KW endoplasmic reticulum; Pseudomonas; exotoxin.

XX OS Synthetic.

XX PN WO9613599-A1.

XX PD 09-MAY-1996.

XX PF 31-OCT-1995; 95WO-EP004270.

XX PR 01-NOV-1994; 94EP-00810627.

XX PA (WELS/) WELS W.

XX PI Wels W, Fominaya J;

XX DR WPI; 1996-239505/24.

XX PT Nucleic acid transfer system for gene therapy, e.g. against cancer -
 PT includes toxin translocation domain to target nucleic acid to specific
 PT cell.

XX PS Disclosure; Page 11; 106pp; English.

XX CC Endoplasmic reticulum retention signals include a mammalian signal
 CC (AAR95063), a bacterial signal (AAT05064) from Pseudomonas exotoxin, and
 CC a yeast signal (AAR95065). The signal may form part of a multidomain
 CC protein (see also AAR95053-58) that is used with an effector nucleic acid
 CC for the transfer of nucleic acids to targeted cells as a means of gene
 CC therapy. The endoplasmic reticulum retention signal functions to affect
 CC intracellular routing of the internalized protein/nucleic acid complex

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 1 REDL 4

RESULT 23

AAR95221

ID AAR95221 standard; protein; 5 AA.

XX AC AAR95221;

XX DT 16-DEC-1996 (first entry)

XX DE Pseudomonas exotoxin C-terminal peptide.

XX KW Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
 KW detection; imaging; immunotoxin; targeting; assay; immunoassay;
 KW Lewis(Y) carbohydrate antigen.

OS	Pseudomonas sp.	PD	01-OCT-1998.
XX		XX	
PN	WO9613594-A1.	PF	24-MAR-1998; 98WO-US005710.
XX		XX	
PD		PR	26-MAR-1997; 97US-0042056P.
XX		XX	
PF		PA	(TEXA) UNIV TEXAS SYSTEM.
XX		XX	
XX	26-OCT-1995; 95WO-US013811.	PI	Draper RK;
XX		XX	
PR	28-OCT-1994; 94US-00331396.	DR	WPI; 1998-532023/45.
PR	28-OCT-1994; 94US-00331397.	XX	
PR	28-OCT-1994; 94US-00331398.	XX	
XX		PT	Delivering compounds to cells as new conjugate with detoxified exotoxin A
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	PT	- able to cross membranes and deliver to the cytoplasm, e.g. nucleic
XX		PT	acids, antibodies, tumour suppressors etc.
XX	Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;	PS	Disclosure; Page 8; 76pp; English.
PI	Fitzgerald D, Brinkmann U, Pai L;	XX	
XX		CC	This peptide is located at the C-terminal end of exotoxin A (ETA, see
DR	WPI; 1996-251462/25.	CC	AAW76391) of Pseudomonas aeruginosa. 4 Of the last 5 amino acids of the
XX		CC	motif are important in the intracellular transport and cytotoxicity of
PT	Single chain fusion proteins and antibodies - useful to diagnose and	CC	ETA. Loss of REDL (see AAW76395) inhibits the ability of ETA to reach the
PT	treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.	CC	cytoplasm. However, REDL can be substituted by KDEL (see AAW76396)
XX		CC	without loss of cytotoxicity. The invention provides a means of
PS	Disclosure; Page 14; 116pp; English.	CC	delivering compounds to cells as conjugates with modified ETA. The
XX		CC	modified ETA is able to cross membranes and deliver e.g. therapeutic
CC	A novel recombinant DNA molecule which encodes a single chain fusion	CC	agents to the cytoplasm such as nucleic acids, peptides, peptide nucleic
CC	protein or antibody comprising the Fv region of both the light and heavy	CC	acids, single chain antibodies and tumour suppressors
CC	chains of an antibody (Ab) fused together, and an effector molecule,	XX	
CC	where the fusion protein or Ab has the binding specificity of monoclonal	SQ	Sequence 5 AA;
CC	Ab (MAB) B1, B3 or B5, can be used for the production of such fusion		
CC	proteins or antibodies. The fusion proteins can be used in compositions	Query Match	100.0%; Score 20; DB 2; Length 5;
CC	as an immunotoxin to inhibit tumour cell growth. The single chain	Best Local Similarity	100.0%; Pred. No. 2e+06;
CC	antibody can be used to detect the presence or absence of cells bearing a	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	Lewis(Y) carbohydrate antigen in a patient. The antibodies are also		
CC	useful as multiple targeting moieties, providing at least 2 kinds of	QY	1 REDL 4
CC	biological activity. They can also be used in diagnostic assays and for		
CC	the imaging of tumours when attached to a radiolabel and for the	Db	1 REDL 4
CC	pathological diagnosis of tumours. Humanised antibodies are less		
CC	immunogenic than the mouse Mabs B1, B3 and B5, making them more suitable	RESULT 25	
CC	for long term treatment. The effector molecule used is preferably a drug	AAW52260	
CC	or cytotoxin which then produces an immunotoxin capable of selectively	ID	AAW52260 standard; peptide; 5 AA.
CC	killing particular cells. Preferred toxins are the Pseudomonas exotoxin	XX	
CC	or Diphtheria toxin. These are both highly toxic compounds and so are	AC	AAW52260;
CC	modified to eliminate domain Ia of the Pseudomonas toxin, various amino	XX	
CC	acid deletions in domains II and III, single amino acid substitutions and	DT	18-JUN-1998 (first entry)
CC	addition of one or more sequences at the C-terminal end	XX	
XX		DE	C-terminal fragment of pseudomonas exotoxin.
SQ	Sequence 5 AA;	XX	
		KW	Pseudomonas exotoxin; PE; cytotoxic.
		XX	
		OS	Pseudomonas sp.
		XX	
		PN	US5705163-A.
		XX	
		PD	06-JAN-1998.
		XX	
		PF	05-JUN-1995; 95US-00461233.
		XX	
		PR	02-JAN-1990; 90US-00459635.
		PR	12-MAY-1990; 90US-00522563.
		XX	
		PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
		XX	
		PI	Fitzgerald D, Pastan I, Chaudhary VK;
		XX	
		DR	WPI; 1998-086092/08.
		XX	
		PT	Methods for killing target cells - with recombinant Pseudomonas exotoxin
		PT	fusion proteins.
		XX	
		PS	Claim 8; Col 14; 12pp; English.

XX This sequence represents a C-terminal fragment of a *Pseudomonas* exotoxin
 CC (PE). This sequence can be used in the method of the invention for
 CC killing a target cell, which comprises contacting the cell with a
 CC recombinant *Pseudomonas* exotoxin (PE) having: (a) a recognition molecule
 CC that binds to the target cell and is inserted in domain III after amino
 CC acid 600 and before amino acid 613 of the PE, and (b) a carboxy-terminal
 CC sequence of 4-16 amino acids that permits translocation of the PE into
 CC the cytosol of the target cell. The insertion of a recognition molecule
 CC allows selective killing of target cells without significant cytotoxicity
 CC to other cells not recognised

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 1 REDL 4

RESULT 26

AAW92909
 ID AAW92909 standard; protein; 5 AA.

XX AC AAW92909;

DT 17-MAY-1999 (first entry)

XX *Pseudomonas* sp. exotoxin A PE ER retention peptide motif #1.

XX Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;
 KW antibody production; non-native epitope; immune response; antigen;
 KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;
 KW secretory; IGA-mediated; mucosal surface; IGA antibody; retention domain;
 KW endoplasmic reticulum.

XX *Pseudomonas* sp.

XX WO9902712-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014336.

XX 11-JUL-1997; 97US-0056924P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX (GETH) GENENTECH INC.

XX Fitzgerald DJ, Mersny RJ;

XX WPI; 1999-120913/10.

XX New *Pseudomonas* exotoxin chimeric immunogens - comprise a foreign epitope
 PT for producing an immune response to pathogens, e.g. virus, bacteria or
 PT protozoa or to cancer antigens.

XX Disclosure; Page 33; 85pp; English.

XX This invention describes a method in which a secretory IGA-mediated
 CC immune response is elicited in a subject. The method involves
 CC administering to at least 1 mucosal surface of the subject a non-toxic
 CC *Pseudomonas* exotoxin A-like (PE-like) chimeric immunogen comprising a
 CC cell recognition domain of that binds to a cell surface receptor on the
 CC mucosal surface, a translocation domain comprising an amino acid sequence
 CC of PE domain II to effect translocation to a cell cytosol, a foreign
 CC epitope domain comprising an amino acid sequence of that encodes a
 CC foreign epitope, and a sequence encoding an endoplasmic reticulum (ER)
 CC retention domain that comprises an ER retention sequence. Also described
 CC is a composition comprising secretory IGA antibodies that specifically

CC recognise an epitope of HIV-1. The method can be used for eliciting an
 CC immune response to pathogens, e.g. virus, bacteria or parasitic protozoa
 CC or to a cancer antigen. The antibodies produced can also be isolated and
 CC used, e.g. for affinity chromatography. The PE immunogens can be made by
 CC wholly recombinant techniques which allows insertion of existing variants
 CC of an epitope, or new variants of rapidly evolving epitopes. The PE can
 CC be engineered to alter the function of its domains, thereby providing a
 CC variety of activities, e.g. by replacing the native cell binding domain
 CC of PE A (domain Ia) with a ligand for a particular cell receptor, the
 CC chimera can be targeted to bind to the particular cell type. By providing
 CC a cell recognition domain that binds to a mucosal surface a secretory
 CC immune response involving IGA can be elicited. This sequence represents a
 CC PE protein endoplasmic reticulum (ER) retention domain motif

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 1 REDL 4

RESULT 27

AAV49697

ID AAV49697 standard; peptide; 5 AA.

XX AC AAV49697;

XX 18-JAN-2000 (first entry)

XX *Pseudomonas* exotoxin peptide #1.

XX *Pseudomonas* exotoxin; PE; mutagenised; IL-13; chimeric; interleukin;
 KW cytotoxin; fusion protein; cancer; glioma; neoplasia.

XX *Pseudomonas* sp.

XX WO9951643-A1.

XX 14-OCT-1999.

XX 31-MAR-1999; 99WO-US007188.

XX 03-APR-1998; 98US-00054711.

XX (PENN-) PENN STATE RES FOUND.

XX Debinski W;

XX WPI; 1999-633731/54.

XX New mutagenized interleukin 13 molecules for delivery of cytotoxins to
 PT cells over expressing IL13 receptors.

XX Disclosure; Page 17; 57pp; English.

XX The present invention describes targeting ligands which are mutagenized
 CC IL13 (interleukin 13) molecules having one or more mutations in the
 CC domain that interacts with the IL13 receptor subunit designated the 140
 CC kDa IL13Rbeta subunit. A cytotoxic molecule covalently attached to a
 CC mutagenized IL13 can be used for delivering an effector molecule to a
 CC cell bearing an IL13 receptor. Where the effector molecule is a
 CC cytotoxin, neoplastic cells (e.g. a glioma) can be killed or inhibited.
 CC The methods are used to target effector molecules to kidney cancers, to
 CC skin cancers (Kaposi's sarcoma) and to brain cancers (gliomas and
 CC medulloblastomas). When the mutagenized cell is attached to a detectable
 CC label the chimeric label can be used to detect the presence or absence of
 CC tumour cells, or localize and/or quantify a cell or cells expressing an
 CC IL13 receptor. The label localizes at the site of overexpression and
 CC indicates the presence, absence, quantity or location of such cells. If

RESULT 30
 AAE33355
 ID AAE33355 standard; peptide; 5 AA.
 AC AAE33355;
 DT 02-APR-2003 (first entry)
 DE Endoplasmic retention peptide #1.
 KW MUC-1; 3D; variable light domain; VL; variable heavy domain; VH; diabody;
 KW cancer; antibody; therapy.
 XX Unidentified.
 OS
 XX WO200279429-A2.
 PN
 XX 10-OCT-2002.
 PD
 XX 28-MAR-2002; 2002WO-US009735.
 PF
 XX 30-MAR-2001; 2001US-0280721P.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA Denardo SJ, Winthrop MD, Denardo GL;
 PI WPI; 2003-046804/04.
 XX
 DR Novel antibody that specifically binds to cancer antigen MUC-1 useful for
 PT detecting a cell bearing MUC-1 antigen, comprises variable light or
 PT variable heavy domains of antibodies 12E, 3D, A5 or C4.
 XX Disclosure; Page 23; 75pp; English.
 PS
 XX The invention relates to a novel antibody that specifically binds to the
 CC cancer antigen MUC-1. The antibody comprises a domain having a sequence
 CC of a polypeptide selected from 12E variable light (VL) or variable heavy
 CC (VH) domain, 3D VL or VH domain, A5 VL or VH domain and C4 VL or VH
 CC domain. Antibodies of the invention are useful for detecting a cell
 CC bearing a MUC-1 antigen. The invention is useful for producing a variety
 CC of human or humanised antibodies or diabodies. The invention is also
 CC useful for treating cancer. The present sequence is endoplasmic retention
 CC peptide, used in the invention
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 20; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 1 REDL 4
 RESULT 31
 ADN07006
 ID ADN07006 standard; peptide; 5 AA.
 AC ADN07006;
 XX 01-JUL-2004 (first entry)
 DT Pseudomonas aeruginosa translocation signalling peptide #1.
 DE Bispecific single chain; bs-scFv; cancer;
 KW epidermal growth factor receptor; EGFR; therapy;
 KW translocation signalling peptide.
 XX Pseudomonas aeruginosa.
 OS

XX US2004071696-A1.
 PN 15-APR-2004.
 PD 04-APR-2003; 2003US-00406830.
 XX 05-APR-2002; 2002US-0370276P.
 PR (REGC) UNIV CALIFORNIA.
 PA (FOXC-) FOX CHASE CANCER CENT.
 XX Adams GP, Horak EM, Weiner LM, Marks JD;
 PI WPI; 2004-328525/30.
 DR
 XX Novel bispecific antibody comprising first and second antibody joined to
 PT each other and having binding specificity to different epitopes of
 PT Epidermal Growth Factor Receptor protein, useful for treating cancer.
 XX Disclosure; SEQ ID NO 23; 57pp; English.
 PS
 XX The present invention provides bispecific single chain (bs-scFv) antibody
 CC molecules which may be used to treat various forms of cancer associated
 CC with the overexpression of the epidermal growth factor receptor (EGFR)
 CC family. The invention is useful for specifically delivering an effector
 CC molecule to a cell bearing a receptor from EGFR protein family chosen
 CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the
 CC treatment of cancer. The present sequence is Pseudomonas aeruginosa
 CC translocation signalling peptide. The peptide is used in the invention.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 20; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 1 REDL 4
 RESULT 32
 ADZ21545
 ID ADZ21545 standard; peptide; 5 AA.
 XX AC ADZ21545;
 XX 30-JUN-2005 (first entry)
 DT Endoplasmic reticulum retention peptide.
 DE
 XX Single chain antibody; MUC-1; tumor-associated antigen; antibody therapy;
 KW cytostatic.
 KW Synthetic.
 OS
 XX WO2005032454-A2.
 PN 14-APR-2005.
 PD 07-MAY-2004; 2004WO-US014159.
 PF 09-MAY-2003; 2003US-00435614.
 XX (REGC) UNIV CALIFORNIA.
 PA Denardo SJ, Winthrop MD, Denardo GL, Xiong C;
 PI WPI; 2005-285319/29.
 DR New antibodies that specifically bind to cancer antigen MUC-1, useful for
 XX tumor targeting, for inhibiting the growth or proliferation of cancer
 PT

PT cells or as diagnostic agents to identify tumors and monitor levels of
PT circulating antigen.
XX Disclosure; SEQ ID NO 11; 79pp; English.
XX
XX The invention provides novel antibodies that specifically bind to the MUC
CC -1 cancer antigen. Preferred single chain antibodies were obtained from a
CC phage display library and were designated as 12E, 3D, A5, C4, B5, E1 and
CC B9 AD221537-AD221543. The heavy chain variable regions (VH) and light
CC chain variable regions (VL) of these antibodies are also provided
CC AD221523-AD221536. The VH and VL domains govern the specificity and
CC binding affinity of the antibodies and permit the construction of a
CC variety of antibodies that specifically target the MUC-1 antigen and
CC cells bearing/displaying the antigen. The antibodies are useful targeting
CC moieties for specifically directing imaging agents and various
CC therapeutic moieties to a cancer. A claimed method of inhibiting the
CC growth or proliferation of a cell bearing a MUC-1 antigen comprises
CC contacting the cell with a chimeric molecule comprising an anti-MUC-1
CC antibody attached to a cytotoxin, a radionuclide, a liposome comprising
CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present
CC sequence is that of an endoplasmic reticulum retention peptide that can
CC be added to the Pseudomonas exotoxin A (PE) moiety of chimeric molecules
CC of the invention. Note: this sequence is referred to as SEQ ID NO:11 on
CC page 24 of the specification, but differs from the sequence given as SEQ
CC ID NO:11 on page 16 AD221533.

XX Sequence 5 AA;
XX
XX Query Match 100.0%; Score 20; DB 9; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 33
AEB27746
ID AEB27746 standard; peptide; 5 AA.
XX
XX AC AEB27746;
XX
XX DT 22-SEP-2005 (first entry)

XX Anti-prostate cancer-antibody related translocation peptide SEQ ID NO 18.
XX
XX DE cytostatic; antibody therapy; pharmaceutical; cancer; metastasis;
XX KW solid tumor; prostate tumor; neoplasm.
XX KW Synthetic.
XX OS
XX PN WO2005062977-A2.
XX PD 14-JUL-2005.
XX PF 21-DEC-2004; 2004WO-US043574.
XX PR 23-DEC-2003; 2003US-0532433P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Liu B, Marks JD;
XX PI WPI; 2005-522452/53.
XX DR
XX PT Novel antibody that specifically binds and is internalized into prostate
XX PT cancer cell, useful for inhibiting growth or proliferation of prostate
XX PT cancer cell and for detecting prostate cancer cell.
XX PS Disclosure; SEQ ID NO 18; 77pp; English.
XX The invention describes an antibody (I) that specifically binds and is

CC internalized into a prostate cancer cell, comprising an antibody that
CC specifically binds an epitope that is specifically bound by an antibody
CC chosen from A33 (SEQ ID No. 22), M10A12 (SEQ ID No. 23), M9B4 (SEQ ID No.
CC 24), OA12 (SEQ ID No. 25), M11G12 (SEQ ID No. 26), M11F12 (SEQ ID No.
CC 27), and C10 (SEQ ID No. 28). Also described are: a chimeric molecule
CC (II), comprising an effector attached to (I); a pharmaceutical
CC formulation (III) comprising an excipient and (I) or (II); detecting (M1)
CC a prostate cancer cell, comprising contacting the prostate cancer cell
CC with (II) attached to an epitope tag, contacting (II) with a chelate
CC comprising a detectable group, where the chelate binds to the epitope tag
CC therefore associating the detectable group with the chelate and detecting
CC the detectable group; a nucleic acid (IV) comprising a nucleic acid that
CC encodes (I); an expression vector (V) comprising (IV); a cell comprising
CC (V); and a kit (VI) comprising a container containing (I), (I) and a
CC chimeric molecule (II) are useful for inhibiting the growth or
CC proliferation of a prostate cancer cell, which involves contacting the
CC cell with (I), or with (II) attached to a cytotoxin or radionuclide. The
CC cell is a metastatic cell or solid tumor cell. (II) is useful for
CC detecting a prostate cancer cell, which involves contacting the prostate
CC cancer cell with (II) attached to a detectable label and detecting the
CC presence or absence of the detectable label. This is the amino acid
CC sequence of a cell membrane translocation peptide used in the creation of
CC single chain anti-prostate cancer-antibodies.

XX Sequence 5 AA;
XX

XX Query Match 100.0%; Score 20; DB 9; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 34
AAW59000
ID AAW59000 standard; peptide; 6 AA.
XX
XX AC AAW59000;
XX
XX DT 30-JUL-1998 (first entry)

XX Human HLA-B27 peptide B27PB derived fragment #4.
XX
XX DE Human leucocyte antigen; HLA; alpha-1 domain; alpha-2 domain; HLA-B27;
XX KW keratin VI; diagnosis; treatment; HLA-dependent autoimmune disease;
XX KW Class I-associated autoimmune disease; iritis; uveitis; psoriasis;
XX KW Class II-associated autoimmune disease; rheumatic disease; arthritis;
XX KW ankylosing spondylitis; antigen; regulator.
XX OS
XX PN Homo sapiens.
XX PD WO9812221-A1.
XX PF 26-MAR-1998.
XX PR 18-SEP-1997; 97WO-EP005124.
XX PR 18-SEP-1996; 96DE-01038108.
XX PA (WILD/) WILDNER G.
XX PI Wildner G;
XX PI WPI; 1998-217206/19.
XX DR
XX PT Treatment and diagnosis of HLA-dependent autoimmune disease - using
XX PT peptide(s) derived from HLA-B27 or human keratin VI, e.g. for iritis,
XX PT uveitis, rheumatic disease etc.
XX PS Disclosure; Page 14; 57pp; German.

AAW58992-W59001 are peptides isolated from the alpha-1 or alpha-2 domain of HLA-B27 or human keratin IV and are used in methods for diagnosis and/or treatment of HLA (human leucocyte antigen)-dependent autoimmune diseases. Such peptides have implications in the treatment of cases of Class I and II-associated autoimmune diseases, especially non-HLA-B27 diseases (iritis, uveitis, psoriasis and rheumatic diseases such as arthritis, psoriatic arthritis or juvenile rheumatoid arthritis) and HLA-B27 diseases e.g. ankylosing spondylitis (AS). These fragments can be administered intravenously, subcutaneously or intramuscularly, or to the mucosa (orally, or as nasal or pulmonary spray). This method results in antigens that are more specific than complete protein antigens, so provide a more exact classification of disease, and thus a more specific treatment. In the case of keratin-derived peptides, they also have better solubility. Compared with complete proteins, peptides are easier to prepare, do not require recovery from natural tissue or recombinant methods of production, have better storage stability when dry, are less likely to cause allergy and have a regulatory effect on the immune system

Sequence 6 AA;

Query Match 100.0%; Score 20; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 3 REDL 6

RESULT 35

AAW58997
 ID AAW58997 standard; peptide; 6 AA.

AC AAW58997;

XX 30-JUL-1998 (first entry)

DE Human HLA-B27 peptide B27PB derived fragment #1.

KW Human leucocyte antigen; HLA; alpha-1 domain; alpha-2 domain; HLA-B27; keratin VI; diagnosis; treatment; HLA-dependent autoimmune disease;
 KW Class I-associated autoimmune disease; iritis; uveitis; psoriasis;
 KW Class II-associated autoimmune disease; rheumatic disease; arthritis; ankylosing spondylitis; antigen; regulator.

XX Homo sapiens.

OS WO9812221-A1.

XX 26-MAR-1998.

XX 18-SEP-1997; 97WO-EP005124.

XX 18-SEP-1996; 96DE-01038108.

XX (WILD/) WILDNER G.

XX Wildner G;

XX WPI; 1998-217206/19.

PT Treatment and diagnosis of HLA-dependent autoimmune disease - using peptide(s) derived from HLA-B27 or human keratin VI, e.g. for iritis, uveitis, rheumatic disease etc.

PS Disclosure; Page 13; 57pp; German.

XX AAW58992-W59001 are peptides isolated from the alpha-1 or alpha-2 domain of HLA-B27 or human keratin IV and are used in methods for diagnosis and/or treatment of HLA (human leucocyte antigen)-dependent autoimmune diseases. Such peptides have implications in the treatment of cases of Class I and II-associated autoimmune diseases, especially non-HLA-B27 diseases (iritis, uveitis, psoriasis and rheumatic diseases such as

CC arthritis, psoriatic arthritis or juvenile rheumatoid arthritis) and HLA-B27 diseases e.g. ankylosing spondylitis (AS). These fragments can be administered intravenously, subcutaneously or intramuscularly, or to the mucosa (orally, or as nasal or pulmonary spray). This method results in antigens that are more specific than complete protein antigens, so provide a more exact classification of disease, and thus a more specific treatment. In the case of keratin-derived peptides, they also have better solubility. Compared with complete proteins, peptides are easier to prepare, do not require recovery from natural tissue or recombinant methods of production, have better storage stability when dry, are less likely to cause allergy and have a regulatory effect on the immune system

Sequence 6 AA;

Query Match 100.0%; Score 20; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 3 REDL 6

RESULT 36

AAW58997
 ID AAW58997 standard; peptide; 6 AA.

AC AAW58997;

XX 24-APR-2001 (first entry)

DE Retroviral recombination assay peptide fragment #7.

KW Retroviral recombination assay; gene therapy vector; viral vector; gag; pol; replication; HIV.

XX Unidentified.

XX WO200104360-A2.

XX 18-JAN-2001.

XX 06-JUL-2000; 2000WO-US018597.

XX 09-JUL-1999; 99US-0143015P.

XX 10-NOV-1999; 99US-0164626P.

XX (UABR-) UAB RES FOUND.

XX (TRAN-) TRANZYME INC.

XX Kappes JC, Wu X, Wakefield J;

XX WPI; 2001-091927/10.

XX N-PSDB; AAF24368.

XX Retroviral recombination assays, systems and cells, useful for evaluating the risk of producing a replication-competent retrovirus from a retroviral-based vector.

XX Example 9; Fig 23; 88pp; English.

XX The present invention describes a method for detecting a retroviral genetic recombinant having gag and pol functions, involving a cell suspected of having a recombinant and propagating the recombinant in the presence of any necessary helper functions. This is useful as it enables the detection of vectors which are able to replicate in the host cell, and allows the production of vectors suitable for gene therapy. The present sequence is a peptide fragment used to demonstrate the method of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 20; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 REDL 4
Db 3 REDL 6

RESULT 37
AAR50265
ID AAR50265 standard; peptide; 7 AA.

AC AAR50265;
XX 25-MAR-2003 (revised)
DT 13-OCT-1994 (first entry)
XX Peptide corresponding to a shared sequence of an HLA molecule.
XX Peptide; HLA; human leucocyte antigen; diagnosis; treatment;
KW autoimmune disease; uveitis; spondylitis; psoriasis;
KW inflammatory bowel disease; enteric bacteria; Klebsiella pneumoniae.
XX Klebsiella pneumoniae.

OS WO9405303-A1.
XX 17-MAR-1994.
XX 31-AUG-1993; 93WO-US008214.
XX 31-AUG-1992; 92US-00944143.
XX (OKLA) UNIV OKLAHOMA STATE.
XX Scofield RH, Harley JB;
XX WPT; 1994-100843/12.
XX Peptide corresponding to shared sequences of HLA molecules and enteric
bacteria - used for the diagnosis and treatment of auto-immune disorders,
partic. spondylarthropathies.
XX Disclosure; Page 41; 58pp; English.
XX The peptide is a fragment of the HLA B27 hypervariable region described
in AAR50266. The peptide can be used for the diagnosis and treatment of
autoimmune disorders, e.g. spondylarthropathies including uveitis and
spondylitis associated with inflammatory bowel disease or psoriasis.
XX (Updated on 25-MAR-2003 to correct PN field.)

QY 1 REDL 4
Db 4 REDL 7

RESULT 38
ADF94279
ID ADF94279 standard; peptide; 7 AA.

AC ADF94279;
XX 26-FEB-2004 (first entry)
DT Human cell protein fragment #4.
XX affinity-labelled RNA; drug discovery; HCV infection; biotin labelled;

KW human.
XX Homo sapiens.

PN US2003194712-A1.
XX 16-OCT-2003.
XX 12-APR-2002; 2002US-00122675.
XX 12-APR-2002; 2002US-00122675.
XX (RIGE-) RIGEL PHARM INC.

PA Lu H, Li W, Anderson D;
XX WPI; 2004-010212/01.
XX Screening for polypeptides that bind to an RNA, useful for treating
hepatitis C virus infection, comprises incubating an affinity-labelled RNA
with a cellular extract, isolating the RNA and identifying polypeptides
bound to the RNA.

XX Example 2; Page 11; 14pp; English.
XX The invention relates to a method of screening for polypeptides that bind
to an RNA comprising incubating an affinity-labelled RNA with a
cytoplasmic extract, where the RNA is linked to an affinity-labelled
oligonucleotide, isolating the affinity-labelled RNA, and identifying
polypeptides bound to the affinity-labelled RNA. The method is useful in
identifying polypeptide factors interacting with RNA. The polypeptide may
be used for drug discovery and in preventing or treating diseases, e.g.
HCV infection. The present sequence represents the amino acid sequence of
a cell protein fragment extracted by a biotinylated hepatitis C virus
IRES.

QY 1 REDL 4
Db 2 REDL 5

Query Match 100.0%; Score 20; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 39
AAR43421
ID AAR43421 standard; peptide; 8 AA.

AC AAR43421;
XX 25-MAR-2003 (revised)
DT 12-MAY-1994 (first entry)
XX La/SSB epitope 246.
XX Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;
KW nuclear ribonucleoprotein; rRNP; Sm B/B'; polypeptide; antigen; D;
KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';
KW RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.

OS Homo sapiens.
XX WO9321223-A1.
XX 28-OCT-1993.
XX 13-APR-1993; 93WO-US003484.
XX 13-APR-1992; 92US-00867819.

PA (OKLA) UNIV OKLAHOMA STATE.

XX Harley JB;

XX WPI; 1993-351658/44.

XX New linear epitope(s) for human auto-antibodies - from the Ro/SSA, La/SSB
PT and Sm B/B' antigens and ribonucleoprotein, used for diagnosing and
PT treating auto-immune disorders e.g. systemic lupus erythematosus.

XX Claim 1; Page 30; 43pp; English.

XX The sequences given in AAR43391-562 are linear epitopes which are derived
CC from the 60 kD Ro/SSA peptide, the La/SSB autoantigen, the 70 kD nuclear
CC ribonucleoprotein (RNP) and the Sm B/B' polypeptide. These antigens are
CC common in systemic lupus erythematosus (SLE) and closely related
CC disorders. The Ro/SSA family of proteins has been shown to have several
CC molecular forms which are defined by the molecular weight of the antigen
CC identified. The major form has a molecular weight of 60 kD and two
CC additional forms have molecular weights of 52 and 54 kD. La/SSB is also a
CC member of this group of autoantibodies and binds small RNAs with a
CC polyuridine terminus. La/SSB is bound by a third of the anti-Ro/SSA
CC precipitin positive sera. La/SSB has been shown to be a 46-50 kD
CC monomeric phosphoprotein which associates with RNA polymerase III
CC transcripts. Anti-Sm antibodies precipitate snRNPs containing the U1, U2,
CC U4/U6 and U5 RNA. Anti-Sm antibodies may be directed against one or a
CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD), E/F
CC (11 kD doublet) and G (less than 10 kD). These epitopes may be used for
CC preventing, treating or screening autoimmune disorders, especially SLE or
CC Sjogrens syndrome (SS). They bind to a human autoantibody and may
CC therefore be used as vaccines. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 20; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 1 REDL 4

RESULT 40

AAW26557
ID AAW26557 standard; peptide; 8 AA.

AC AAW26557;

XX 16-JAN-1998 (first entry)

DE Soluble peptide inhibitor of retroviral protease.

XX Retrovirus; gag-pol; protease; transframe region; inhibitor;
KW human immunodeficiency virus type 1; HIV-1; infection; therapy;
KW antiviral agent; virucide; screening; antibody; vaccine.

XX Synthetic.

XX WO9712907-A1.

XX 10-APR-1997.

XX 24-SEP-1996; 96WO-US015304.

XX 05-OCT-1995; 95US-00539432.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Medabalimi JL;

XX WPI; 1997-226161/20.

XX

PT New peptide from trans-frame region of retroviral protein - useful for
PT inhibiting activity and maturation of retroviral, esp. HIV, protease,
PT e.g. for treatment of infection and for screening for antiviral agents.

XX Claim 3; Page 37; 53pp; English.

XX 17 Claimed peptides comprise the peptides given in AAW26557-61 as well as
CC the dipeptides Asp-Asp, Asp-Glu and Asp-Gln and the tripeptides Glu-Asp-
CC Leu, Arg-Glu-Asp, Asp-Glu-Leu, Glu-Glu-Leu, Asp-Asp-Leu, Glu-Asn-Leu, Glu-
CC Lys-Phe, Glu-Asp-Phe and Asp-Asp-Phe. They are derived from, or related
CC to, a claimed peptide (see AAW26556) from the transframe region (TFR) of
CC HIV-1 Gag-Pol polyprotein. Also claimed are: antibodies (Ab) reactive
CC with the TFR peptide; and (3) anti-idiotypic antibodies (AAb) reactive
CC retroviral, especially HIV-1, protease activity (and also block protease
CC maturation) so can be used: (1) to treat cells infected with retrovirus;
CC (2) to screen for other compounds having similar antiviral activity; (3)
CC to stabilise retroviral compositions, especially vaccines, against
CC proteolysis; (4) to screen compounds for more general inhibition of
CC aspartyl proteases; and (5) to inhibit other aspartyl proteases. Since
CC the peptides competitively inhibit protease and block its maturation,
CC they should not lead to rapid selection of viral variants that are
CC resistant

XX Sequence 8 AA;

Query Match 100.0%; Score 20; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 3 REDL 6

RESULT 41

ABP15821

XX ABP15821 standard; peptide; 8 AA.

AC ABP15821;

XX 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A24 super motif pol peptide #1.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.

XX Claim 32; Page 193; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 3 REDL 6

CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 3 REDL 6

RESULT 42
ABP21200
ID ABP21200 standard; peptide; 8 AA.
XX
AC ABP21200;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif pol peptide #195.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 304; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

RESULT 43
ABP24221
ID ABP24221 standard; peptide; 8 AA.
XX
AC ABP24221;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 motif pol peptide #29.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 365; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CII and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 8 AA;
Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 3 REDL 6

RESULT 44
AAAY66341
ID AAAY66341 standard; peptide; 9 AA.

AC AAAY66341;

DT 12-SEP-2003 (revised)
DT 22-FEB-2000 (first entry)

DE HLA-A24-binding HIV-1 Pol peptide #143.

XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;
KW human leukocyte antigen; allele; binding; conserved; genome; peptide;
KW targeting; toxic; drug; antibody; antigen; antiviral;
KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;
KW localisation; quantification; detection; infection; drug resistance;
KW immune response.

XX Human immunodeficiency virus 1.

OS WO9949893-A1.

PN 07-OCT-1999.

XX 31-MAR-1999; 99WO-US007111.

XX 31-MAR-1998; 98US-00052530.

XX (UWBO-) UNIV BOSTON.

PA Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;

PI WPI; 2000-038361/03.

XX Novel methods for designing molecular conjugate therapeutics which are used for diagnosis, imaging and treatment against pathogens.

PS Example 3; Page 45; 62pp; English.

XX AAAY66199-Y66413 are peptides derived from conserved portions of the HIV-1 genome which bind to different HLA alleles of MHC (major histocompatibility complex) Class I molecules. The peptides are used to construct targeting antigens comprising one or more peptides bound to

CC the corresponding MHC Class I molecule, which can be used to raise
CC antibodies. The antibody may then be used as a targeting vehicle to
CC deliver a potentially toxic drug to its target site of action, rather
CC than administering it systemically, which may result in adverse side
CC effects. The invention relates to improved methods for the design of
CC molecular conjugate therapeutics for the diagnosis and treatment of
CC infections caused by pathogens with a high mutation rate (such as HIV-1).
CC This method involves identifying conserved peptide-encoding regions among
CC the genomes of multiple variants of a pathogen, identifying the Class I
CC MHC molecules which occur with greatest frequency in a population of
CC interest (e.g., human sub-populations), and determining which of the
CC peptides bind to the Class I MHC molecules. The MHC-binding peptides and
CC the corresponding Class I MHC molecules are selected and used to
CC construct targeting antigens, which are in turn used to produce
CC targeting antibodies. The methods may be used in localisation,
CC quantification and in situ detection of specific peptide-MHC Class I
CC complexes and also to detect and treat viral infection. The methods of
CC the invention mitigate against the development of viral resistance to
CC drugs and to the immune response, as well as providing a solution for
CC targeting toxic compounds to destroy viruses sequestered in sites not
CC accessible to T cells. In addition, the methods eliminate the virus,
CC whereas current therapies only arrest viral replication. (Updated on 12-
CC SEP-2003 to standardise OS field)

XX Sequence 9 AA;

Query Match 100.0%; Score 20; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 3 REDL 6

RESULT 45
AAB35211

ID AAB35211 standard; peptide; 9 AA.

XX AAB35211;

XX 24-APR-2001 (first entry)

XX Retroviral recombination assay peptide fragment #9.

XX Retroviral recombination assay; gene therapy vector; viral vector; gag;
KW pol; replication; HIV.

XX Unidentified.

XX WO200104360-A2.

XX 18-JAN-2001.

XX 06-JUL-2000; 2000WO-US018597.

XX 09-JUL-1999; 99US-0143015P.

XX 10-NOV-1999; 99US-0164626P.

XX (UABR-) UAB RES FOUND.

XX (TRAN-) TRANZYME INC.

XX Kappes JC, Wu X, Wakefield J;

XX WPI; 2001-091927/10.

XX N-PSDB; AAF24370.

XX Retroviral recombination assays, systems and cells, useful for evaluating
XX the risk of producing a replication-competent retrovirus from a
XX retroviral-based vector.

XX Example 10; Fig 24; 88pp; English.

CC The present invention describes a method for detecting a retroviral
CC genetic recombinant having gag and pol functions, involving a cell
CC suspected of having a recombinant and propagating the recombinant in the
CC presence of any necessary helper functions. This is useful as it enables
CC the detection of vectors which are able to replicate in the host cell,
CC and allows the production of vectors suitable for gene therapy. The
CC present sequence is a peptide fragment used to demonstrate the method of
CC the invention
XX

XX Sequence 9 AA;

Query Match 100.0%; Score 20; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 6 REDL 9

RESULT 46
AEB87899
ID AEB87899 standard; peptide; 9 AA.

XX AC AEB87899;

XX DT 20-OCT-2005 (first entry)

XX DE Klebsiella aerogenes pullulanase PUL1 conserved fragment II.

XX KW carbohydrolase; LSA; hydrolysis; starch; polysaccharide; decontamination;
XX KW tooth disease; sugar; antibacterial; pullulanase; PUL1.

XX OS Klebsiella aerogenes.

XX PN WO2005073369-A1.

XX PD 11-AUG-2005.

XX PF 27-JAN-2005; 2005WO-KR000235.

XX PR 30-JAN-2004; 2004KR-00006186.

XX PA (LIFE-) LIFENZA CO LTD.

XX PI Kang H, Lee J;

XX DR WPI; 2005-555696/56.

XX PT New proteins that hydrolyze amylopectin, starch, glycogen or amylose,
XX PT useful for removing dextran or polysaccharide contaminants during sugar
XX PT production, or for eliminating plaques or as mouthwash.

XX PS Example 4; Page 18; 42pp; English.

XX CC This invention describes a novel carbohydrolase AEB87861 which is capable
XX CC of hydrolyzing amylopectin, starch, glycogen or amylose, or its
XX CC derivative or fragment. The invention also describes 1) a gene, or its
XX CC derivative or fragment, comprising AEB87862 which encodes AEB87861 or its
XX CC derivative or fragment; 2) a transformed prokaryotic or eukaryotic cell
XX CC expressing AEB87862 or its derivative or fragment e.g. Escherichia coli
XX CC B121 (DES) plysS deposited with the accession number of KCTC10573HP; 3) a
XX CC method of producing an enzyme having activity of hydrolyzing amylopectin,
XX CC starch, glycogen or amylose; 4) an enzyme produced by the method of 3)
XX CC and 5) a composition comprising the enzyme. The composition and methods
XX CC are useful for removing dextran or polysaccharide contaminants during
XX CC sugar production. The novel enzyme inhibits the formation of dental
XX CC plaque and eliminates previously formed plaque and this anticaries
XX CC activity is useful for anti-plaque compositions or mouthwashes. This
XX CC sequence represents a conserved region of Klebsiella aerogenes
XX CC pullulanase PUL1.

XX Sequence 9 AA;

Query Match 100.0%; Score 20; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 3 REDL 6

RESULT 47

AEB87903

ID AEB87903 standard; peptide; 9 AA.

XX AC AEB87903;

XX DT 20-OCT-2005 (first entry)

XX DE G. stearothermophilus pullulanase PUL2 conserved fragment II.

XX KW carbohydrolase; LSA; hydrolysis; starch; polysaccharide; decontamination;
XX KW tooth disease; sugar; antibacterial; pullulanase; PUL2.

XX OS Geobacillus stearothermophilus.

XX PN WO2005073369-A1.

XX PD 11-AUG-2005.

XX PF 27-JAN-2005; 2005WO-KR000235.

XX PR 30-JAN-2004; 2004KR-00006186.

XX PA (LIFE-) LIFENZA CO LTD.

XX PI Kang H, Lee J;

XX DR WPI; 2005-555696/56.

XX PT New proteins that hydrolyze amylopectin, starch, glycogen or amylose,
XX PT useful for removing dextran or polysaccharide contaminants during sugar
XX PT production, or for eliminating plaques or as mouthwash.

XX PS Example 4; Page 18; 42pp; English.

XX CC This invention describes a novel carbohydrolase AEB87861 which is capable
XX CC of hydrolyzing amylopectin, starch, glycogen or amylose, or its
XX CC derivative or fragment. The invention also describes 1) a gene, or its
XX CC derivative or fragment, comprising AEB87862 which encodes AEB87861 or its
XX CC derivative or fragment; 2) a transformed prokaryotic or eukaryotic cell
XX CC expressing AEB87862 or its derivative or fragment e.g. Escherichia coli
XX CC B121 (DES) plysS deposited with the accession number of KCTC10573HP; 3) a
XX CC method of producing an enzyme having activity of hydrolyzing amylopectin,
XX CC starch, glycogen or amylose; 4) an enzyme produced by the method of 3)
XX CC and 5) a composition comprising the enzyme. The composition and methods
XX CC are useful for removing dextran or polysaccharide contaminants during
XX CC sugar production. The novel enzyme inhibits the formation of dental
XX CC plaque and eliminates previously formed plaque and this anticaries
XX CC activity is useful for anti-plaque compositions or mouthwashes. This
XX CC sequence represents a conserved region of Geobacillus stearothermophilus
XX CC pullulanase PUL2.

XX Sequence 9 AA;

Query Match 100.0%; Score 20; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 3 REDL 6

RESULT 48

AE87895
ID AEB87895 standard; peptide; 9 AA.

XX
AC AEB87895;

XX
DT 20-OCT-2005 (first entry)

XX
DE Pseudomonas amyloclavata isoamylase IAM conserved fragment II.

XX
KW carboxylase; LSA; hydrolysis; starch; polysaccharide; decontamination;
XX
KW tooth disease; sugar; antibacterial; isoamylase; IAM.

XX
OS Pseudomonas amyloclavata.

XX
PN WO2005073369-A1.

XX
PD 11-AUG-2005.

XX
PF 27-JAN-2005; 2005WO-KR000235.

XX
PR 30-JAN-2004; 2004KR-00006186.

XX
PA (LIFE-) LIFENZA CO LTD.

XX
PI Kang H, Lee J;

XX
DR WPI; 2005-555696/56.

XX
PT New proteins that hydrolyze amylopectin, starch, glycogen or amylose,
XX
PT useful for removing dextran or polysaccharide contaminants during sugar
XX
PT production, or for eliminating plaques or as mouthwash.

XX
PS Example 4; Page 18; 42pp; English.

XX
CC This invention describes a novel carboxylase AEB87861 which is capable
XX
CC of hydrolyzing amylopectin, starch, glycogen or amylose, or its
XX
CC derivative or fragment. The invention also describes 1) a gene, or its
XX
CC derivative or fragment, comprising AEB87862 which encodes AEB87861 or its
XX
CC derivative or fragment; 2) a transformed prokaryotic or eukaryotic cell
XX
CC expressing AEB87862 or its derivative or fragment e.g. Escherichia coli
XX
CC B121 (DE3) pLysS deposited with the accession number of KCTC10573HP; 3) a
XX
CC method of producing an enzyme having activity of hydrolyzing amylopectin,
XX
CC starch, glycogen or amylose; 4) an enzyme produced by the method of 3)
XX
CC and 5) a composition comprising the enzyme. The composition and methods
XX
CC are useful for removing dextran or polysaccharide contaminants during
XX
CC sugar production. The novel enzyme inhibits the formation of dental
XX
CC plaque and eliminates previously formed plaque and this anticaries
XX
CC activity is useful for anti-plaque compositions or mouthwashes. This
XX
CC sequence represents a conserved region of Pseudomonas amyloclavata
XX
CC isoamylase IAM.

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db |||||

3 REDL 6

RESULT 49

AE41212
ID AAR41212 standard; peptide; 10 AA.

XX
AC AAR41212;

XX
XX 25-MAR-2003 (revised)

XX
DT 15-MAR-1994 (first entry)

XX
DE Peptide fragment of Class I HLA peptide.

XX

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.

XX
OS Synthetic.

XX
PN WO9317699-A1.

XX
PD 16-SEP-1993.

XX
PF 25-FEB-1993; 93WO-US001758.

XX
PR 02-MAR-1992; 92US-00844716.

XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX
PI Clayberger CA, Krensky AM;

XX
DR WPI; 1993-303134/38.

XX
PT New peptide(s) based on Class I HLA antigen domains - used for modulating
XX
PT cytotoxic T-lymphocyte activity towards targets.

XX
PS Claim 11; Page 54; 61pp; English.

XX
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity,
XX
CC either by inhibition or stimulation. It can be used for inhibiting CTL
XX
CC toxicity in transplantations, for inducing CTL activity in parasitic
XX
CC diseases and neoplasia and in studies on viral infection. The peptide can
XX
CC also be used for identifying CTLs which bind to it and removing subsets
XX
CC of CTLs from a T-cell composition. This peptide sequence is more commonly
XX
CC found within larger peptide compounds of not more than 30 amino acids in
XX
CC length. (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db |||||

1 REDL 4

RESULT 50

AE83075
ID AAR83075 standard; peptide; 10 AA.

XX
AC AAR83075;

XX
DT 16-MAY-1996 (first entry)

XX
DE HLA-B2702 CTL modulating peptide (B2702.75-84).

XX
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
XX
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
XX
KW Class I MHC; HLA-B2702.

XX
OS Synthetic.

XX
PN WO9526979-A1.

XX
PD 12-OCT-1995.

XX
PF 05-APR-1995; 95WO-US004349.

XX
PR 05-APR-1994; 94US-00222851.

XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX
PI Clayberger C, Krensky AM, Parham P;

DR WPI; 1995-358582/46.
XX PT Extension of acceptance period of transplants from MHC unmatched donor
PT hosts - using Class I B*5-84 MHC antigen of the recipient host.
XX PS
XX Example 14; Page 34; 80pp; English.
XX
CC AAR81061-R83085, AAR81090-R83096 and AAR92907-R92913 represent fragments
CC of class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 20; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDL 4
Db 1 REDL 4
Search completed: March 20, 2006, 07:52:26
Job time : 80.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:51:44 ; Search time 18.5 Seconds
(without alignments)
17.876 Million cell updates/sec

Title: US-09-673-707-10
Perfect score: 20
Sequence: 1 REDL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	4	1	US-08-405-615-15
2	20	100.0	4	1	US-08-331-398A-52
3	20	100.0	4	1	US-08-461-234-15
4	20	100.0	4	1	US-08-463-480-15
5	20	100.0	4	1	US-08-821-840-3
6	20	100.0	4	1	US-08-665-202-27
7	20	100.0	4	1	US-08-809-668-13
8	20	100.0	4	1	US-08-331-397B-52
9	20	100.0	4	1	US-08-759-804A-52
10	20	100.0	4	2	US-08-722-258-60
11	20	100.0	4	2	US-09-397-951-13
12	20	100.0	4	2	US-08-776-271-5
13	20	100.0	4	2	US-09-047-148-11
14	20	100.0	4	2	US-09-215-035-5
15	20	100.0	4	2	US-09-479-479-34
16	20	100.0	4	2	US-09-297-851-34
17	20	100.0	4	2	US-09-315-574-27
18	20	100.0	4	2	US-08-913-370-3
19	20	100.0	4	2	US-09-581-345-9
20	20	100.0	4	4	PCT-US93-12078-4
21	20	100.0	5	1	US-08-405-615-14
22	20	100.0	5	1	US-08-331-398A-53
23	20	100.0	5	1	US-08-082-849B-33
24	20	100.0	5	1	US-08-406-192-20
25	20	100.0	5	1	US-08-461-234-14
26	20	100.0	5	1	US-08-545-151-20
27	20	100.0	5	1	US-08-463-480-14
28	20	100.0	5	1	US-08-821-840-2
29	20	100.0	5	1	US-08-665-202-26
30	20	100.0	5	1	US-08-809-668-8
31	20	100.0	5	1	US-08-331-397B-53
32	20	100.0	5	1	US-08-759-804A-53
33	20	100.0	5	2	US-08-722-258-59
34	20	100.0	5	2	US-08-722-258-65
35	20	100.0	5	2	US-09-397-951-8
36	20	100.0	5	2	US-08-776-271-4
37	20	100.0	5	2	US-09-047-148-10
38	20	100.0	5	2	US-09-215-035-4
39	20	100.0	5	2	US-09-479-479-33
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49	20	100.0	10	1	US-08-222-851-14
50	20	100.0	10	1	US-08-222-851-30
51	20	100.0	10	1	US-08-440-504A-5
52	20	100.0	10	2	US-08-651-650-13
53	20	100.0	10	2	US-08-651-650-15
54	20	100.0	10	2	US-08-651-650-37
55	20	100.0	10	2	US-09-028-083B-36
56	20	100.0	10	4	PCT-US94-12985-9
57	20	100.0	14	1	US-08-962-284-8
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59	20	100.0	14	2	US-08-433-613-7
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61	20	100.0	16	1	US-08-539-432-19
62	20	100.0	16	4	PCT-US93-08214-16
63	20	100.0	17	1	US-08-105-416-29
64	20	100.0	17	1	US-08-105-416-30
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67	20	100.0	17	2	US-08-483-931B-29
68	20	100.0	17	2	US-08-483-931B-30
69	20	100.0	18	1	US-08-651-835A-15
70	20	100.0	19	2	US-09-671-089-4
71	20	100.0	21	2	US-09-367-953B-22
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73	20	100.0	25	4	PCT-US94-12985-13
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75	20	100.0	26	2	US-10-324-616A-23
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87	20	100.0	59	2	US-09-513-999C-6526
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96	20	100.0	74	2	US-08-311-731A-296
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Sequence 4935, Ap
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Sequence 1952, Ap
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Sequence 51, Appl
Sequence 15637, A
Sequence 263, App
Sequence 6, Appli
Sequence 4131, Ap

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||||
Db 1 REDL 4

US-08-331-398A-52
Sequence 52, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331.398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

US-08-405-615-15
Sequence 15, Application US/08405615
Patent No. 5602095
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Fitzgerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ellen L. Weber
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:

; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-398A-52

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 3
US-08-461-234-15
; Sequence 15, Application US/08461234
; Patent No. 5821238
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Fitzgerald, David J.
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
; TITLE OF INVENTION: Increased Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/461,234
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,709
; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,615
; FILING DATE: 15-MAR-1995
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-461-234-15

Query Match 100.0%; Score 20; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 REDL 4
Db 1 REDL 4
RESULT 4
US-08-463-480-15
; Sequence 15, Application US/08463480
; Patent No. 5854044
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Fitzgerald, David J.
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
; TITLE OF INVENTION: Increased Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,480
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,709
; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,615
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-463-480-15

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 5
US-08-821-840-3
; Sequence 3, Application US/08821840
; Patent No. 5919456
; GENERAL INFORMATION:
; APPLICANT: Puri, Raj K.
; APPLICANT: Debinski, Waldemar

Mon Mar 20 08:51:25 2006

APPLICANT: Pastan, Ira
APPLICANT: Obiri, Nicholas
TITLE OF INVENTION: IL-13 Receptor Specific Chimeric
TITLE OF INVENTION: Proteins and Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,840
FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,685
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-217100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-821-840-3

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 6
US-08-665-202-27
Sequence 27, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-27

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 7

US-08-809-668-13
Sequence 13, Application US/08809668
Patent No. 5980895
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Kuan, Chien-Tsun
TITLE OF INVENTION: Immunotoxin Containing a
TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a
TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 5980895 Require Proteolytic
TITLE OF INVENTION: Activation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,668
FILING DATE: 21-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,388
FILING DATE: 13-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16327
FILING DATE: 11-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-253100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-809-668-13

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 8
US-08-331-397B-52
; Sequence 52, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-397B-52

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 1 REDL 4
||||

RESULT 9
US-08-759-804A-52
; Sequence 52, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-759-804A-52

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 10
US-08-722-258-60
; Sequence 60, Application US/08722258
; Patent No. 6011002
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira

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us-09-673-707-10.ra1

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; APPLICANT: Kreitman, Robert J.
; APPLICANT: Puri, Raj K.
; TITLE OF INVENTION: Circularly Permuted Ligands and
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,258
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/04468
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,224
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-193100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-722-258-60

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 11
US-09-397-951-13
; Sequence 13, Application US/09397951
; Patent No. 6074644
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kuan, Chien-Tsun
; TITLE OF INVENTION: Immunotoxin Containing a
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 6074644 Require Proteolytic
; TITLE OF INVENTION: Activation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,271
; FILING DATE: 01-DEC-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; US-09-397-951-13

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 12
US-08-776-271-5
; Sequence 5, Application US/08776271
; Patent No. 6083502
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,271
; FILING DATE: 01-DEC-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; US-09-397-951-13

```

REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-259100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-776-271-5

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 13
US-09-047-148-11
Sequence 11, Application US/09047148
Patent No. 6086900
GENERAL INFORMATION:
APPLICANT: Draper, Rockford
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
TITLE OF INVENTION: CELL MEMBRANES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,148
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,056
FILING DATE: 26-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSF-072
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-9577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-047-148-11

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

Db 1 REDL 4
RESULT 14
US-09-215-035-5
Sequence 5, Application US/09215035
Patent No. 6153430
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Chang, Kai
TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,035
FILING DATE: No. 6153430 yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/776,271
FILING DATE: 01-DEC-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/00224
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,166
FILING DATE: 05-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-259110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-215-035-5

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 15
US-09-479-479-34
Sequence 34, Application US/09479479
Patent No. 6423513
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:

;; TITLE OF INVENTION: Protease-Activatable Pseudomonas
;; TITLE OF INVENTION: Exotoxin A-Like Proteins
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/479,479
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/297,851
;; FILING DATE: 30-JUL-1999
;; APPLICATION NUMBER: US 60/030,376
;; FILING DATE: 06-NOV-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/20207
;; FILING DATE: 05-NOV-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015280-29810US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-479-479-34

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4
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|||

RESULT 16
US-09-297-851-34
; Sequence 34, Application US/09297851
; Patent No. 6426075
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Protease-Activatable Pseudomonas
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/297,851
;; FILING DATE: 30-JUL-1999
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/030,376
;; FILING DATE: 06-NOV-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/20207
;; FILING DATE: 05-NOV-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015280-29810US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-297-851-34

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4
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RESULT 17
US-09-315-574-27
; Sequence 27, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-27

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
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Db 1 REDL 4

RESULT 18
US-08-913-370-3
Sequence 3, Application US/08913370
Patent No. 6518061
GENERAL INFORMATION:
APPLICANT: Puri, Raj K.
APPLICANT: Debinski, Waldemar
APPLICANT: Pastan, Ira
APPLICANT: Obiri, Nicholas
TITLE OF INVENTION: IL-13 Receptor Specific Chimeric
TITLE OF INVENTION: Proteins and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,370
FILING DATE: 17-FEB-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,685
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/03486
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-217110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-913-370-3

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
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|
|
Db 1 REDL 4

RESULT 19
US-09-581-345-9
Sequence 9, Application US/09581345
Patent No. 6809184
GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
APPLICANT: Chowdhury, Partha S.
APPLICANT: The Government of the United States
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Antibodies, Including Fv Molecules, and
TITLE OF INVENTION: Immunocjugates Having High Binding Affinity for
TITLE OF INVENTION: Mesothelin and Methods for Their Use
FILE REFERENCE: 015280-339100US
CURRENT APPLICATION NUMBER: US/09/581,345
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/067,175
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: WO PCT/US98/25270
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:carboxyl
OTHER INFORMATION: terminus
US-09-581-345-9

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
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|
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Db 1 REDL 4

RESULT 20
PCT-US93-12078-4
Sequence 4, Application PC/TUS9312078
GENERAL INFORMATION:
APPLICANT: NAME: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS
APPLICANT: SYSTEM: 201 West 7th Street
APPLICANT: CITY: Austin
APPLICANT: STATE: Texas
APPLICANT: COUNTRY: United States of America
APPLICANT: POSTAL CODE: 78701
APPLICANT: TELEPHONE NO: (512)499-4462
APPLICANT: TELEFAX: (512)499-4523
TITLE OF INVENTION: POTENT AND SPECIFIC
TITLE OF INVENTION: CHEMICALLY-CONJUGATED
TITLE OF INVENTION: IMMUNOTOXINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON

; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12078
; FILING DATE: UNKNOWN
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/992,900
; FILING DATE: 16.12.92
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTFF046PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2676
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-12078-4

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 21
US-08-405-615-14
; Sequence 14, Application US/08405615
; Patent No. 5602095
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: FitzGerald, David J.
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
; TITLE OF INVENTION: Increased Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ellen L. Weber
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,615
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-405-615-14

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 22
US-08-331-398A-53
; Sequence 53, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-398A-53

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
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Db 1 REDL 4

RESULT 23

US-08-082-849B-33
; Sequence 33, Application US/08082849B
; Patent No. 5677274
; GENERAL INFORMATION:
; APPLICANT: Lepplia, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Arora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
; TITLE OF INVENTION: Related Methods
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,849B
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,601
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-161-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-082-849B-33

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|
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|
|
Db 1 REDL 4

RESULT 24

US-08-406-192-20
; Sequence 20, Application US/08406192
; Patent No. 5739287
; GENERAL INFORMATION:
; APPLICANT: Wilbur, D. Scott
; APPLICANT: Prathare, Pradip M
; TITLE OF INVENTION: Biotinylated Cobalamins
; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101-2333
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,192
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,831
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Renzoni, George E
; REGISTRATION NUMBER: 37,919
; REFERENCE/DOCKET NUMBER: RECL18947
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-192-20

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|
|
|
|
Db 1 REDL 4

RESULT 25

US-08-461-234-14
; Sequence 14, Application US/08461234
; Patent No. 5821238
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Fitzgerald, David J.
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
; TITLE OF INVENTION: Increased Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,234
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,709

TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
TELEX: 4938023
APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
US-08-545-151-20

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 27
US-08-463-480-14
Sequence 14, Application US/08463480
Patent No. 5854044
GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
APPLICANT: Fitzgerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,480
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,709
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-463-480-14

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA: US 08/405,615
APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-461-234-14

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 26
US-08-545-151-20
Sequence 20, Application US/08545151
Patent No. 5840712
GENERAL INFORMATION:
APPLICANT: Morgan Jr, A. Charles
APPLICANT: Wilbur, D. Scott
APPLICANT: Prathare, Pradip M
TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor
TITLE OF INVENTION: Modulating Agents and Methods Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson & KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: WA 98101-2333
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,151
FILING DATE: 19-OCT-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04404
FILING DATE: 07-APR-1995
APPLICATION NUMBER: US 08/406,192
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: US 08/406,194
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: US 08/406,191
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: US 08/224,831
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Renzoni, George E
REGISTRATION NUMBER: 37,919
REFERENCE/DOCKET NUMBER: RECL18878
TELECOMMUNICATION INFORMATION:

Qy 1 REDL 4
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Db 1 REDL 4

RESULT 28

US-08-821-840-2
; Sequence 26, Application US/08821840
; Patent No. 5919456
; GENERAL INFORMATION:
; APPLICANT: Puri, Raj K.
; APPLICANT: Debinski, Waldemar
; APPLICANT: Pastan, Ira
; APPLICANT: Obiri, Nicholas
; TITLE OF INVENTION: IL-13 Receptor Specific Chimeric
; TITLE OF INVENTION: Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,840
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,685
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-217100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-821-840-2

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|
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|
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Db 1 REDL 4

RESULT 29

US-08-665-202-26
; Sequence 26, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322a1 High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-26

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|
|
|
|
Db 1 REDL 4

RESULT 30

US-08-809-668-8
; Sequence 8, Application US/08809668
; Patent No. 5980895
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kuan, Chien-Tsun
; TITLE OF INVENTION: Immunotoxin Containing a
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 5980895 Require Proteolytic
; TITLE OF INVENTION: Activation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,668
; FILING DATE: 21-AUG-1997

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-397B-53

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 32
US-08-759-804A-53
; Sequence 53, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-759-804A-53

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 1 REDL 4

RESULT 33
US-08-722-258-59
; Sequence 59, Application US/08722258
; Patent No. 6011002
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kreitman, Robert J.
; APPLICANT: Puri, Raj K.
; TITLE OF INVENTION: Circularly Permuted Ligands and
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,258
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/04468
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,224
; FILING DATE: 08-APR-1994
; NAME: Weber, Ellen Lauver
; ATTORNEY/AGENT INFORMATION:
; FILING DATE: 08-APR-1994
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-193100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-722-258-59

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 1 REDL 4

RESULT 34
US-08-722-258-65
; Sequence 65, Application US/08722258
; Patent No. 6011002
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kreitman, Robert J.
; APPLICANT: Puri, Raj K.

; TITLE OF INVENTION: Circularly Permuted Ligands and
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,258
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/04468
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,224
; FILING DATE: 08-APR-1994
; NAME: Weber, Ellen Lauver
; ATTORNEY/AGENT INFORMATION:
; FILING DATE: 08-APR-1994
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-193100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-722-258-65

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 1 REDL 4

RESULT 35
US-09-397-951-8
; Sequence 8, Application US/09397951
; Patent No. 6074644
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kuan, Chien-Tsun
; TITLE OF INVENTION: Immunotoxin Containing a
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 6074644 Require Proteolysis
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/397,951
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,668
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16327
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-253100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-397-951-8

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4

RESULT 36
US-09-776-271-4
; Sequence 4, Application US/08776271
; Patent No. 6083502
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,271
; FILING DATE: 01-DEC-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-259100US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-776-271-4

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4

RESULT 37
US-09-047-148-10
; Sequence 10, Application US/09047148
; Patent No. 6086900
; GENERAL INFORMATION:
; APPLICANT: Draper, Rockford
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; TITLE OF INVENTION: CELL MEMBRANES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,148
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,056
; FILING DATE: 26-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSP-072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-047-148-10

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4
```


RESULT 38

US-09-215-035-4
; Sequence 4, Application US/09215035
; Patent No. 6153430
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,035
; FILING DATE: No. 6153430 yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/776,271
; FILING DATE: 01-DEC-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-259110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-215-035-4

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 39

US-09-479-479-33
; Sequence 33, Application US/09479479
; Patent No. 6423513
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Protease-Activatable Pseudomonas
; TITLE OF INVENTION: Exotoxin A-Like Proteins

NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/297,851
; FILING DATE: 30-JUL-1999
; APPLICATION NUMBER: US 60/030,376
; FILING DATE: 06-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/20207
; FILING DATE: 05-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015280-29810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-479-479-33

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 40

US-09-297-851-33
; Sequence 33, Application US/09297851
; Patent No. 6426075
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Protease-Activatable Pseudomonas
; TITLE OF INVENTION: Exotoxin A-Like Proteins
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/297,851
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,376
; FILING DATE: 06-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/20207
; FILING DATE: 05-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015280-29810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-297-851-33

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 41
US-08-840-713-46
; Sequence 46, Application US/08840713
; Patent No. 6498233
; GENERAL INFORMATION:
; APPLICANT: WELS, Winfried, Dr.
; APPLICANT: FOYMINAVA, Jesus
; TITLE OF INVENTION: NUCLEIC ACID TRANSFER SYSTEM
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., N.W., Suite 330 - G St. Lobby
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,713
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kittle, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1614-7014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638 - 5000
; TELEFAX: (202) 638 - 4810
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-297-851-33

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 42
US-09-315-574-26
; Sequence 26, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-26

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 43
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US-08-913-370-2
; Sequence 2, Application US/08913370
; Patent No. 6518061
; GENERAL INFORMATION:
; APPLICANT: Puri, Raj K.
; APPLICANT: Debinski, Waldemar
; APPLICANT: Pastan, Ira
; APPLICANT: Obiri, Nicholas
; TITLE OF INVENTION: IL-13 Receptor Specific Chimeric
; TITLE OF INVENTION: Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,370
; FILING DATE: 17-FEB-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,685
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/03486
; FILING DATE: 15-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-217110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-913-370-2

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 44
US-10-122-675-6
; Sequence 6, Application US/10122675
; Patent No. 6927031
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Li, Weiqun
; APPLICANT: Lu, Henry
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying Polypeptide Factors Interacting
; TITLE OF INVENTION: With RNA
; FILE REFERENCE: 021044-002000US
; CURRENT APPLICATION NUMBER: US/10/122,675
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:40S ribosomal
; OTHER INFORMATION: protein S18 peptide
US-10-122-675-6

Query Match 100.0%; Score 20; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 2 REDL 5

RESULT 45
PCT-US93-08214-15
; Sequence 15, Application PC/TUS9308214
; GENERAL INFORMATION:
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: Peptide Diagnostics and Therapeutics for Spondyloarthropath
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: United States
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08214
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRf138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Klebsiella pneumoniae
PCT-US93-08214-15

Query Match 100.0%; Score 20; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 4 REDL 7

RESULT 46

Mon Mar 20 08:51:25 2006

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US-08-539-432-1
; Sequence 1, Application US/08539432
; Patent No. 5872210
; GENERAL INFORMATION:
; APPLICANT: MEDABALIMI, JOHN L.
; TITLE OF INVENTION: TRANSFRAME INHIBITORY
; TITLE OF INVENTION: ELEMENT OF VIRAL
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,432
; FILING DATE: 05-OCT-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-539-432-1

Query Match 100.0%; Score 20; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 47
US-08-475-955-33
; Sequence 33, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; TITLE OF INVENTION: AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,955
; FILING DATE: June 7, 1995

US-07-867-819D-33
; Sequence 33, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
; FILE REFERENCE: OMRF 114 CIP (2)
; CURRENT APPLICATION NUMBER: US/07/867,819D
; CURRENT FILING DATE: 1992-04-13
; PRIOR APPLICATION NUMBER: 07/472,947
; PRIOR FILING DATE: 1990-01-31
; PRIOR APPLICATION NUMBER: 07/648,205
; PRIOR FILING DATE: 1991-01-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Binding site
; US-07-867-819D-33

Query Match 100.0%; Score 20; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 48
US-07-867-819D-33
; Sequence 33, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
; FILE REFERENCE: OMRF 114 CIP (2)
; CURRENT APPLICATION NUMBER: US/07/867,819D
; CURRENT FILING DATE: 1992-04-13
; PRIOR APPLICATION NUMBER: 07/472,947
; PRIOR FILING DATE: 1990-01-31
; PRIOR APPLICATION NUMBER: 07/648,205
; PRIOR FILING DATE: 1991-01-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Binding site
; US-07-867-819D-33

Query Match 100.0%; Score 20; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

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RESULT 49
US-08-222-851-14
; Sequence 14, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-851-14

Query Match 100.0%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 50
US-08-222-851-30
; Sequence 30, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-851-30

Query Match 100.0%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

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Gapop 10.0 , Gapext 0.5												
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Maximum Match 100%												
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	2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*											
	3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*											
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2	20	100.0	4	3	US-09-462-713-12	Sequence 12, Appl	30	20	100.0	19	4	US-10-126-845-62
3	20	100.0	4	4	US-10-112-788-16	Sequence 16, Appl	31	20	100.0	19	4	US-10-116-275-92
4	20	100.0	4	4	US-10-297-337-16	Sequence 16, Appl	32	20	100.0	19	4	US-10-764-235-4
5	20	100.0	4	4	US-10-406-830-24	Sequence 24, Appl	33	20	100.0	19	5	US-10-955-656-4
6	20	100.0	4	4	US-10-432-412-22	Sequence 22, Appl	34	20	100.0	19	5	US-10-955-656-62
7	20	100.0	4	4	US-10-432-412-23	Sequence 23, Appl	35	20	100.0	20	3	US-09-864-761-39759
8	20	100.0	4	4	US-10-363-233-7	Sequence 7, Appli	36	20	100.0	20	4	US-10-136-187-5
9	20	100.0	4	5	US-10-659-036-12	Sequence 12, Appl	37	20	100.0	20	4	US-10-136-187-9
10	20	100.0	4	5	US-10-490-535-6	Sequence 6, Appli	38	20	100.0	20	5	US-10-850-873-5
11	20	100.0	4	5	US-10-973-718-9	Sequence 9, Appli	39	20	100.0	20	5	US-10-850-873-9
12	20	100.0	4	6	US-11-021-438-19	Sequence 19, Appl	40	20	100.0	20	5	US-10-690-276-239
13	20	100.0	5	3	US-09-480-236-6	Sequence 6, Appli	41	20	100.0	21	4	US-10-302-547-89
14	20	100.0	5	3	US-09-462-713-11	Sequence 11, Appl	42	20	100.0	21	4	US-10-302-547-90
15	20	100.0	5	4	US-10-112-788-15	Sequence 15, Appl	43	20	100.0	23	4	US-10-029-386-32550
16	20	100.0	5	4	US-10-297-337-15	Sequence 15, Appl	44	20	100.0	26	6	US-11-155-043-23
17	20	100.0	5	4	US-10-406-830-23	Sequence 23, Appl	45	20	100.0	26	6	US-09-864-761-37447
18	20	100.0	5	4	US-10-432-412-21	Sequence 21, Appl	46	20	100.0	28	3	US-09-864-761-42724
19	20	100.0	5	5	US-10-659-036-11	Sequence 11, Appl	47	20	100.0	28	3	US-10-808-187-236
20	20	100.0	5	5	US-10-490-535-7	Sequence 7, Appli	48	20	100.0	28	5	US-10-807-807-236
21	20	100.0	5	6	US-11-021-438-18	Sequence 18, Appl	49	20	100.0	28	5	US-10-807-807-236
22	20	100.0	7	4	US-10-122-675-6	Sequence 6, Appli	50	20	100.0	31	3	US-09-932-367A-33
23	20	100.0	8	4	US-10-137-867-296	Sequence 296, App	51	20	100.0	33	4	US-10-425-115-269508
24	20	100.0	8	4	US-10-376-121A-33	Sequence 33, Appl	52	20	100.0	35	4	US-10-012-542-324
25	20	100.0	9	4	US-10-133-210-114	Sequence 114, App	53	20	100.0	35	4	US-10-115-123-324
26	20	100.0	10	5	US-10-780-321-40	Sequence 40, Appl	54	20	100.0	35	4	US-10-424-599-159103
27	20	100.0	11	3	US-09-955-504-29	Sequence 29, Appl	55	20	100.0	36	4	US-10-800-834-324
							56	20	100.0	36	4	US-10-424-599-242042
							57	20	100.0	36	5	US-10-896-169-3
							58	20	100.0	37	6	US-11-077-752-15
							59	20	100.0	38	4	US-10-437-963-195320
							60	20	100.0	38	4	US-10-425-115-287477
							61	20	100.0	38	6	US-11-077-752-14
							62	20	100.0	39	3	US-09-864-761-43161
							63	20	100.0	40	4	US-10-424-599-256593
							64	20	100.0	41	4	US-10-425-115-273706
							65	20	100.0	41	4	US-10-425-115-205956
							66	20	100.0	42	4	US-10-425-115-230741
							67	20	100.0	43	4	US-10-424-599-269749
							68	20	100.0	43	4	US-10-425-115-332906
							69	20	100.0	43	5	US-10-450-763-30799
							70	20	100.0	44	3	US-09-873-637-28
							71	20	100.0	44	4	US-10-264-049-4105
							72	20	100.0	44	4	US-10-424-599-231706
							73	20	100.0	44	4	US-10-437-963-174698
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							75	20	100.0	45	4	US-10-767-701-54557
							76	20	100.0	46	4	US-10-425-115-319937
							77	20	100.0	47	3	US-09-864-761-45129
							78	20	100.0	47	4	US-10-424-599-214990
							79	20	100.0	47	4	US-10-424-599-249770
							80	20	100.0	47	4	US-10-437-963-198312
							81	20	100.0	47	4	US-10-425-115-201052
							82	20	100.0	47	4	US-10-425-115-293536
							83	20	100.0	48	4	US-10-424-599-177161
							84	20	100.0	49	3	US-09-864-761-47908
							85	20	100.0	49	4	US-10-029-386-31181
							86	20	100.0	49	4	US-10-029-386-33086
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							94	20	100.0	52	4	US-10-424-599-257365
							95	20	100.0	52	4	US-10-437-963-115604
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101	20	100.0	53	4	US-10-425-115-186409	Sequence 186409,
102	20	100.0	53	4	US-10-425-115-347598	Sequence 347598,
103	20	100.0	54	3	US-09-864-761-35507	Sequence 35507, A
104	20	100.0	54	4	US-10-029-386-30385	Sequence 30385, A
105	20	100.0	55	3	US-09-874-472-14	Sequence 14, Appl
106	20	100.0	55	3	US-09-874-472-15	Sequence 15, Appl
107	20	100.0	55	4	US-10-424-599-188608	Sequence 188608,
108	20	100.0	56	3	US-09-764-869-741	Sequence 741, App
109	20	100.0	56	4	US-10-091-504-741	Sequence 741, App
110	20	100.0	56	4	US-10-106-698-7718	Sequence 7718, App
111	20	100.0	56	4	US-10-227-577-741	Sequence 741, App
112	20	100.0	56	4	US-10-424-599-258318	Sequence 258318,
113	20	100.0	56	4	US-10-437-963-113850	Sequence 113850,
114	20	100.0	56	4	US-10-425-115-267206	Sequence 267206,
115	20	100.0	57	4	US-10-042-865-135	Sequence 135, App
116	20	100.0	57	4	US-10-042-865-168	Sequence 168, App
117	20	100.0	57	4	US-10-425-115-249559	Sequence 249559,
118	20	100.0	58	4	US-10-029-386-28462	Sequence 28462, A
119	20	100.0	58	4	US-10-425-115-300873	Sequence 300873,
120	20	100.0	58	5	US-10-450-763-36788	Sequence 36788, A
121	20	100.0	59	3	US-09-867-550-1378	Sequence 1378, Ap
122	20	100.0	59	3	US-09-864-408A-1182	Sequence 1182, Ap
123	20	100.0	59	4	US-10-437-963-166446	Sequence 166446,
124	20	100.0	59	4	US-10-437-963-187600	Sequence 187600,
125	20	100.0	60	3	US-09-864-761-37408	Sequence 37408, A
126	20	100.0	60	3	US-09-864-761-39057	Sequence 39057, A
127	20	100.0	60	3	US-09-796-692-2305	Sequence 2305, Ap
128	20	100.0	60	4	US-10-040-862-2305	Sequence 2305, Ap
129	20	100.0	60	4	US-10-105-004-21	Sequence 21, Appl
130	20	100.0	60	4	US-10-105-004-24	Sequence 24, Appl
131	20	100.0	60	4	US-10-057-4758-2305	Sequence 2305, Ap
132	20	100.0	60	4	US-10-154-884B-2305	Sequence 2305, Ap
133	20	100.0	60	4	US-10-764-324-2305	Sequence 2305, Ap
134	20	100.0	61	4	US-10-424-599-196613	Sequence 196613,
135	20	100.0	61	4	US-10-424-599-225935	Sequence 225935,
136	20	100.0	61	4	US-10-387-346B-148	Sequence 148, App
137	20	100.0	61	4	US-10-437-963-103492	Sequence 103492,
138	20	100.0	61	4	US-10-686-947-148	Sequence 148, App
139	20	100.0	61	4	US-10-425-115-226180	Sequence 226180,
140	20	100.0	61	5	US-10-943-507-148	Sequence 190881,
141	20	100.0	62	4	US-10-424-599-190881	Sequence 190881,
142	20	100.0	62	4	US-10-437-963-202743	Sequence 202743,
143	20	100.0	62	4	US-10-425-115-336662	Sequence 336662,
144	20	100.0	63	4	US-10-424-599-240757	Sequence 240757,
145	20	100.0	63	4	US-10-424-599-254364	Sequence 254364,
146	20	100.0	63	4	US-10-767-701-47748	Sequence 47748, A
147	20	100.0	63	4	US-10-425-115-233371	Sequence 233371,
148	20	100.0	63	4	US-10-425-115-248387	Sequence 248387,
149	20	100.0	63	4	US-10-425-115-284208	Sequence 284208,
150	20	100.0	64	4	US-10-425-115-281585	Sequence 281585,

ALIGNMENTS

RESULT 1

US-09-480-236-7

;

FEATURE:

;

OTHER INFORMATION: Description of Artificial Sequence: PE peptide

US-09-480-236-7

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 REDL 4

|||||

Db

1 REDL 4

RESULT 2

US-09-462-713-12

;

Sequence 12, Application US/09462713

;

Publication No. US20030054012A1

;

GENERAL INFORMATION:

;

APPLICANT: FitzGerald, David J.

;

APPLICANT: Msnny, Randall J.

;

APPLICANT: The Government of the United States of America

;

APPLICANT: Genentech, Inc.

;

TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens

;

TITLE OF INVENTION: for Elicitinga Secretary IgA-Mediated Immune Response

;

FILE REFERENCE: 015280-361100US

;

CURRENT APPLICATION NUMBER: US/09/462,713

;

CURRENT FILING DATE: 2000-05-12

;

PRIOR APPLICATION NUMBER: PCT/US98/14336

;

PRIOR FILING DATE: 1998-07-10

;

PRIOR APPLICATION NUMBER: US 60/056,924

;

PRIOR FILING DATE: 1997-07-11

;

NUMBER OF SEQ ID NOS: 13

;

SOFTWARE: PatentIn Ver. 2.0

;

SEQ ID NO 12

;

LENGTH: 4

;

TYPE: PRT

;

ORGANISM: Artificial Sequence

;

FEATURE:

;

OTHER INFORMATION: Description of Artificial Sequence: endoplasmic

;

OTHER INFORMATION: reticulum (ER) retention sequence

US-09-462-713-12

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 REDL 4

|||||

Db

1 REDL 4

RESULT 3

US-10-112-788-16

;

Sequence 16, Application US/10112788

;

Publication No. US20030077676A1

;

GENERAL INFORMATION:

;

APPLICANT: DENARDO, SALLY

;

APPLICANT: WINTHROP, MICHELLE

;

APPLICANT: DENARDO, GERALD

;

TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING

;

FILE REFERENCE: 309T-000210US

;

CURRENT APPLICATION NUMBER: US/10/112,788

;

CURRENT FILING DATE: 2002-03-28

;

PRIOR APPLICATION NUMBER: US 60/280,721

;

PRIOR FILING DATE: 2001-04-30

;

NUMBER OF SEQ ID NOS: 19

;

SOFTWARE: PatentIn version 3.0

;

SEQ ID NO 16

;

LENGTH: 4

;

TYPE: PRT

;

ORGANISM: Artificial Sequence

;

FEATURE:

;

OTHER INFORMATION: Recombinant translocation peptide

US-10-112-788-16

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 REDL 4

|||||

Db

1 REDL 4

US-10-112-788-16

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 1 REDL 4

RESULT 4

US-10-297-337-16
; Sequence 16, Application US/10297337
; Publication No. US20040018203A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Tautsumi, Yasuo
; APPLICANT: Onda, Masanori
; APPLICANT: Nagata, Satoshi
; APPLICANT: Lee, Byungkook
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: PEGylation of Linkers Improves Antitumor Activity and
; TITLE OF INVENTION: Reduces Toxicity of Immunoconjugates
; FILE REFERENCE: 015280-423200US
; CURRENT APPLICATION NUMBER: US/10/297,337
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/211,331
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/213,804
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: WO PCT/US01/18503
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal
; OTHER INFORMATION: variation to maintain ability of construct to
; OTHER INFORMATION: translocate to cytosol
US-10-297-337-16

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 1 REDL 4

RESULT 5

US-10-406-830-24
; Sequence 24, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05

; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Translocation signaling sequence.
US-10-406-830-24

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 1 REDL 4

RESULT 6

US-10-432-412-22
; Sequence 22, Application US/10432412
; Publication No. US20040071731A1
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain
US-10-432-412-22

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 1 REDL 4

RESULT 7

US-10-432-412-23
; Sequence 23, Application US/10432412
; Publication No. US20040071731A1
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21

```

; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for
; FILE REFERENCE: 015280-361200US
; CURRENT APPLICATION NUMBER: US/10/659,036
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 09/462,713
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-10-659-036-12

Query Match      100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
DB      1 REDL 4

RESULT 10
US-10-490-535-6
; Sequence 6, Application US/10490535
; Publication No. US20050118182A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Beers, Richard
; APPLICANT: Kreiman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100US
; CURRENT APPLICATION NUMBER: US/10/490,535
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: WO PCT/US02/30316
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: carboxyl
; OTHER INFORMATION: terminus addition to maintain ability of the
; OTHER INFORMATION: construct to translocate to cytosol
US-10-490-535-6

Query Match      100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
DB      1 REDL 4

; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for
; FILE REFERENCE: 015280-361200US
; CURRENT APPLICATION NUMBER: US/10/659,036
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 09/462,713
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain
US-10-432-412-23

Query Match      100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
DB      1 REDL 4

RESULT 8
US-10-363-233-7
; Sequence 7, Application US/10363233
; Publication No. US2004008772A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Liu, Xiu Fen
; APPLICANT: Bera, Tapan K.
; APPLICANT: Lee, Byungkook
; APPLICANT: Eglund, Kristi A.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: XAGB-1, a Gene Expressed in Multiple Cancers, and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 015280-420100US
; CURRENT APPLICATION NUMBER: US/10/363,233
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/229,684
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: WO PCT/US01/27258
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Pseudomonas
; OTHER INFORMATION: exotoxin carboxy terminus addition
US-10-363-233-7

Query Match      100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
DB      1 REDL 4

RESULT 9
US-10-659-036-12
; Sequence 12, Application US/10659036
; Publication No. US2005007917A1
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: Mrsny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the

```

RESULT 11
US-10-973-718-9
; Sequence 9, Application US/10973718
; Publication No. US20050214304A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Chowdhury, Partha S.
; APPLICANT: The Government of the United States
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Antibodies, including Fv Molecules, and
; TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity for
; TITLE OF INVENTION: Mesothelin and Methods for Their Use
; FILE REFERENCE: 015280-339100US
; CURRENT APPLICATION NUMBER: US/10/973,718
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US/09/581,345
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/067,175
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: carboxyl
US-10-973-718-9

Query Match 100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 1 REDL 4

RESULT 12
US-11-021-438-19
; Sequence 19, Application US/11021438
; Publication No. US20050186214A1
; GENERAL INFORMATION:
; APPLICANT: LIU, BIN
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: PROSTATE CANCER SPECIFIC INTERNALIZING HUMAN ANTIBODIES
; FILE REFERENCE: 407T-392710US
; CURRENT APPLICATION NUMBER: US/11/021,438
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/532,433
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide translocation signal sequence.
US-11-021-438-19

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||

RESULT 13
US-09-480-236-6
; Sequence 6, Application US/09480236
; Patent No. US20020142000A1
; GENERAL INFORMATION:
; APPLICANT: Digan, Mary Ellen
; APPLICANT: Lake, Philip
; APPLICANT: Wright, Richard M.
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
; FILE REFERENCE: CGC 4-31157A/USN
; CURRENT APPLICATION NUMBER: US/09/480,236
; CURRENT FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PE peptide
US-09-480-236-6

Query Match 100.0%; Score 20; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 1 REDL 4

RESULT 14
US-09-462-713-11
; Sequence 11, Application US/09462713
; Publication No. US20030054012A1
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: Mersny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
; FILE REFERENCE: 015280-361100US
; CURRENT APPLICATION NUMBER: US/09/462,713
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-09-462-713-11

Query Match 100.0%; Score 20; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 1 REDL 4

RESULT 15
US-09-462-713-11

US-10-112-788-15
; Sequence 15, Application US/10112788
; Publication No. US20030077676A1
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY
; APPLICANT: WINTHROP, MICHELLE
; APPLICANT: DENARDO, GERALD
; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
; FILE REFERENCE: 309T-000210US
; CURRENT APPLICATION NUMBER: US/10/112,788
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,721
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant translocation peptide
US-10-112-788-15

Query Match 100.0%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 16
US-10-297-337-15
; Sequence 15, Application US/10297337
; Publication No. US20040018203A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Tsutsumi, Yasuo
; APPLICANT: Onda, Masanori
; APPLICANT: Nagata, Satoshi
; APPLICANT: Lee, Byungkook
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: PEGylation of Linkers Improves Antitumor Activity and
; TITLE OF INVENTION: Reduces Toxicity of Immunoconjugates
; FILE REFERENCE: 015280-43200US
; CURRENT APPLICATION NUMBER: US/10/297,337
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/211,331
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/213,804
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: WO PCT/US01/18503
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PE38 C-terminal
; OTHER INFORMATION: native residues 609-613
US-10-297-337-15

Query Match 100.0%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4

Db 1 REDL 4

RESULT 17
US-10-406-830-23
; Sequence 23, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Translocation signaling sequence.
US-10-406-830-23

Query Match 100.0%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 18
US-10-432-412-21
; Sequence 21, Application US/10432412
; Publication No. US20040071731A1
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain in native
; OTHER INFORMATION: Pseudomonas exotoxin A
US-10-432-412-21

Query Match 100.0%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 REDL 4
Db 1 REDL 4

RESULT 19
US-10-659-036-11
; Sequence 11, Application US/10659036
; Publication No. US20050079171A1
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: Msnny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for
; TITLE OF INVENTION: Eliciting a Secretory IGA-Mediated Immune Response
; FILE REFERENCE: 015280-361200US
; CURRENT APPLICATION NUMBER: US/10/659,036
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 09/462,713
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-10-659-036-11

Query Match 100.0%; Score 20; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 20
US-10-490-535-7
; Sequence 7, Application US/10490535
; Publication No. US20050118182A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Salvatore, Giuliana
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100US
; CURRENT APPLICATION NUMBER: US/10/490,535
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: WO PCT/US02/30316
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT

Query Match 100.0%; Score 20; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 21
US-11-021-438-18
; Sequence 18, Application US/11021438
; Publication No. US20050186214A1
; GENERAL INFORMATION:
; APPLICANT: LIU, BIN
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: PROSTATE CANCER SPECIFIC INTERNALIZING HUMAN ANTIBODIES
; FILE REFERENCE: 407T-392710US
; CURRENT APPLICATION NUMBER: US/11/021,438
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/532,433
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide translocation signal sequence.
US-11-021-438-18

Query Match 100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 22
US-10-122-675-6
; Sequence 6, Application US/10122675
; Publication No. US20030194712A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Li, Weiqun
; APPLICANT: Lu, Henry
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying Polypeptide Factors Interacting
; TITLE OF INVENTION: With RNA
; FILE REFERENCE: 021044-002000US
; CURRENT APPLICATION NUMBER: US/10/122,675
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 40S ribosomal
; OTHER INFORMATION: protein S18 peptide
US-10-122-675-6

Query Match 100.0%; Score 20; DB 4; Length 7;
```

```
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 2 REDL 5

RESULT 23
US-10-137-867-296
; Sequence 296, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 296
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-296

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 5 REDL 8

RESULT 24
US-10-376-121A-33
; Sequence 33, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-376-121A-33

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 25
US-10-133-210-114
; Sequence 114, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-114

Query Match 100.0%; Score 20; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 3 REDL 6
```

RESULT 26
US-10-780-321-40
; Sequence 40, Application US/10780321
; Publication No. US2004024810A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Grassy, Gerard
; APPLICANT: Calas, Bernard
; TITLE OF INVENTION: Cycomodulating Lipophilic Peptides for Modulating Immune System
; FILE REFERENCE: A-64360-2/TAL/CYO (465840-00087)
; CURRENT APPLICATION NUMBER: US/10/780,321
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 09/028,083
; PRIOR FILING DATE: 1998-02-28
; PRIOR APPLICATION NUMBER: US 08/838,916
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-780-321-40

Query Match 100.0%; Score 20; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 27
US-09-955-504-29
; Sequence 29, Application US/09955504
; Publication No. US20020182702A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/955,504
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,222
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 09/712,907
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: PCT/US00/14308
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/178,717
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/142,930
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/136,388
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-504-29

Query Match 100.0%; Score 20; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 8 REDL 11
RESULT 28
US-10-125-452-29
; Sequence 29, Application US/10125452
; Publication No. US20020173640A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT006P2
; CURRENT APPLICATION NUMBER: US/10/125,452
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/955,504
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 09/712,907
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: PCT/US00/14308
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/178,717
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/142,930
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/136,388
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-452-29

Query Match 100.0%; Score 20; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 8 REDL 11

RESULT 29
US-10-126-845-4
; Sequence 4, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-10-126-845-4

Query Match 100.0%; Score 20; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 16 REDL 19

RESULT 32
US-10-764-235-4
; Sequence 4, Application US/10764235
; Publication No. US20040138132A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: P26,479-B USA
; CURRENT APPLICATION NUMBER: US/10/764,235
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
; US-10-764-235-4
Query Match 100.0%; Score 20; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 REDL 4
Db 16 REDL 19
RESULT 33
US-10-955-656-4
; Sequence 4, Application US/10955656
; Publication No. US20050101762A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALS
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/10/955,656
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
; US-10-955-656-4
Query Match 100.0%; Score 20; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 REDL 4
Db 16 REDL 19

US-10-126-845-62
; Sequence 62, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)_(19)
; OTHER INFORMATION: D form amino acid
; US-10-126-845-62
Query Match 100.0%; Score 20; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 REDL 4
Db 16 REDL 19
RESULT 31
US-10-116-275-92
; Sequence 92, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Up
; OTHER INFORMATION: take Across the GIT"
; US-10-116-275-92
Query Match 100.0%; Score 20; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 REDL 4
Db 16 REDL 19


```

RESULT 34
US-10-955-656-62
; Sequence 62, Application US/10955656
; Publication No. US20050101762A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/10/955,656
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(19)
; OTHER INFORMATION: D form amino acid
US-10-955-656-62

Query Match 100.0%; Score 20; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 16 REDL 19

RESULT 35
US-09-864-761-39759
; Sequence 39759, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39759
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005332.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EST_HUMAN HIT: AI076293.1, EVALUATE 1.00e-05
US-09-864-761-39759

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 10 REDL 13

RESULT 36
US-10-136-187-5
; Sequence 5, Application US/10136187
; Publication No. US20030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/136,187
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct

```

```
US-10-136-187-5
Query Match      100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      17 REDL 20

RESULT 37
US-10-136-187-9
; Sequence 9, Application US/10136187
; Publication No. US20030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-136-187-9

Query Match      100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      17 REDL 20

RESULT 38
US-10-850-873-5
; Sequence 5, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-850-873-5

Query Match      100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      17 REDL 20

RESULT 39
US-10-850-873-9
; Sequence 9, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-850-873-9

Query Match      100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      17 REDL 20

RESULT 40
US-10-690-276-239
; Sequence 239, Application US/10690276
; Publication No. US20050112118A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Cimbora, Daniel
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul
; APPLICANT: Mauck, Kimberly
; APPLICANT: Bush, Angie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
; FILE REFERENCE: 1834.01
; CURRENT APPLICATION NUMBER: US/10/690,276
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/727,384
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/168,377
```

```
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/168,379
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/185,056
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 10/035,344
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,571
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/035,343
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,572
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/099,924
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,179
; PRIOR FILING DATE: 2001-03-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 728
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-690-276-239

Query Match      100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 REDL 4
Db      1 REDL 4
```

```
RESULT 41
US-10-302-547-89
; Sequence 89, Application US/10302547
; Publication No. US20040142448A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, BRIAN R.
; APPLICANT: COLLINS, PETER L.
; APPLICANT: SKIADOPOULOS, MARIO H.
; APPLICANT: NEWMAN, JASON T.
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE
; TITLE OF INVENTION: 1 (HP1V1) FROM CDNA AND USE OF RECOMBINANT HP1V1 IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT
; TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 2303-37-3
; CURRENT APPLICATION NUMBER: US/10/302,547
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/331,961
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Human parainfluenza virus 3
US-10-302-547-89
```

```
Query Match      100.0%; Score 20; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 REDL 4
Db      15 REDL 18
```

```
RESULT 42
US-10-302-547-90
; Sequence 90, Application US/10302547
```

```
; Publication No. US20040142448A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, BRIAN R.
; APPLICANT: COLLINS, PETER L.
; APPLICANT: SKIADOPOULOS, MARIO H.
; APPLICANT: NEWMAN, JASON T.
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE
; TITLE OF INVENTION: 1 (HP1V1) FROM CDNA AND USE OF RECOMBINANT HP1V1 IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT
; TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 2303-37-3
; CURRENT APPLICATION NUMBER: US/10/302,547
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/331,961
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 90
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Human parainfluenza virus 3
US-10-302-547-90
```

```
Query Match      100.0%; Score 20; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 REDL 4
Db      15 REDL 18
```

```
RESULT 43
US-10-029-386-32550
; Sequence 32550, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AROMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32550
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002472.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: SWISSPROT HIT: O43246, EVALUE 2.00e-06
US-10-029-386-32550
```

```
Query Match      100.0%; Score 20; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 REDL 4
Db      18 REDL 21
```

```
RESULT 44
US-11-155-043-23
```

Sequence 23. Application US/11155043	Sequence 23. Application US/11155043
Publication No. US20050238629A1	Publication No. US20050238629A1
GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited	APPLICANT: Oxford Biomedica (UK) Limited
APPLICANT: Kingseman, Alan John	APPLICANT: Kingseman, Alan John
APPLICANT: Kingseman, Susan Mary	APPLICANT: Kingseman, Susan Mary
TITLE OF INVENTION: Therapeutic Gene	TITLE OF INVENTION: Therapeutic Gene
FILE REFERENCE: 674523-2015	FILE REFERENCE: 674523-2015
CURRENT APPLICATION NUMBER: US/11/155,043	CURRENT APPLICATION NUMBER: US/11/155,043
CURRENT FILING DATE: 2005-06-17	CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US/10/324,616	PRIOR APPLICATION NUMBER: US/10/324,616
PRIOR FILING DATE: 2002-12-20	PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 09/254,832	PRIOR APPLICATION NUMBER: US 09/254,832
PRIOR FILING DATE: 1999-06-21	PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: PCT/GB97/02969	PRIOR APPLICATION NUMBER: PCT/GB97/02969
PRIOR FILING DATE: 1997-10-28	PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: GB 9622500.8	PRIOR APPLICATION NUMBER: GB 9622500.8
PRIOR FILING DATE: 1996-10-29	PRIOR FILING DATE: 1996-10-29
NUMBER OF SEQ ID NOS: 28	NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2	SOFTWARE: PatentIn version 3.2
SEQ ID NO 23	SEQ ID NO 23
LENGTH: 26	LENGTH: 26
TYPE: PRT	TYPE: PRT
ORGANISM: Saccharomyces cerevisiae	ORGANISM: Saccharomyces cerevisiae
US-11-155-043-23	US-11-155-043-23
Query Match	Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 26;	Best Local Similarity 100.0%; Score 20; DB 6; Length 26;
Mismatches 0; Indels 0; Gaps 0;	Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;	Matches 4; Conservative 0; Mismatches 0;
QY 1 REDL 4	QY 1 REDL 4
DB 6 REDL 9	DB 6 REDL 9
RESULT 45	RESULT 45
US-09-864-761-37447	US-09-864-761-37447
Sequence 37447, Application US/09864761	Sequence 37447, Application US/09864761
Patent No. US20020048763A1	Patent No. US20020048763A1
GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.	APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.	APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.	APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng	APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR	TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY	TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aemica-X-1	FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761	CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23	CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312	PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04	PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456	PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26	PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366	PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03	PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6	PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04	PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359	PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27	PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666	PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667	PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664	PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669	PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665	PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668	PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663	PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669	PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666	PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667	PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664	PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669	PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666	PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667	PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664	PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669	PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666	PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30	PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667	PRIOR APPLICATION NUMBER: PCT/US01/0

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42724
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050342.29
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EST_HUMAN HIT: F08485.1, EVALUATE 2.00e-09
US-09-864-761-42724

Query Match 100.0%; Score 20; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 18 REDL 21

RESULT 47
US-10-808-187-236
; Sequence 236, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10808.187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 236
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-236

Query Match 100.0%; Score 20; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 6 REDL 9

RESULT 49

; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 236
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-236

Query Match 100.0%; Score 20; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 6 REDL 9

RESULT 48
US-10-807-807-236
; Sequence 236, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 236
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-236

Query Match 100.0%; Score 20; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 6 REDL 9

RESULT 49

Mon Mar 20 08:51:25 2006

```
US-09-932-367A-33
; Sequence 33, Application US/09932367A
; Publication No. US20030027152A1
; GENERAL INFORMATION:
; APPLICANT: RHODES, Simon J.
; APPLICANT: BRIDWELL, Jeanne L.
; APPLICANT: MEIER, Bradley C.
; APPLICANT: PARKER, Gretchen E.
; APPLICANT: PRICE, Jeffrey R.
; APPLICANT: SHOWALTER, Aaron D.
; APPLICANT: SLOOP, Kyle W.
; TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
; FILE OF INVENTION: LHX3/P-LIM/LIM-3 FACTOR
; FILE REFERENCE: 053884-5003
; CURRENT APPLICATION NUMBER: US/09/932,367A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/04424
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/121,110
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-932-367A-33

Query Match      100.0%; Score 20; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      26 REDL 29

RESULT 50
US-10-425-115-269508
; Sequence 269508, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 269508
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177387C.1.pep
US-10-425-115-269508

Query Match      100.0%; Score 20; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      22 REDL 25

Search completed: March 20, 2006, 07:55:14
Job time : 64.5 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:53:30 ; Search time 8.5 Seconds
(without alignment)
13.470 Million cell updates/sec

Title: US-09-673-707-10
Perfect score: 20
Sequence: 1 REDL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

Published Applications_AA_New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	6	US-10-537-061-12
2	20	100.0	4	7	US-11-019-027-16
3	20	100.0	7	7	US-11-096-706-24
4	20	100.0	8	7	US-11-045-024-4306
5	20	100.0	8	7	US-11-045-024-9685
6	20	100.0	8	7	US-11-045-024-12706
7	20	100.0	11	6	US-10-892-870-3
8	20	100.0	11	6	US-10-938-690-3
9	20	100.0	28	7	US-11-004-399-929
10	20	100.0	37	6	US-10-729-121-15
11	20	100.0	38	6	US-10-729-121-15
12	20	100.0	55	7	US-11-140-311-14
13	20	100.0	55	7	US-11-140-311-15
14	20	100.0	60	6	US-10-475-075-913
15	20	100.0	61	6	US-10-934-944-148
16	20	100.0	61	7	US-11-116-881A-157
17	20	100.0	72	6	US-10-544-501-8
18	20	100.0	75	7	US-11-096-568A-4959
19	20	100.0	82	7	US-11-124-367A-275
20	20	100.0	82	7	US-11-124-367A-277
21	20	100.0	82	7	US-11-124-367A-278
22	20	100.0	82	7	US-11-124-367A-279
23	20	100.0	99	7	US-11-087-099-6823
24	20	100.0	100	6	US-10-793-626-2944
25	20	100.0	112	6	US-10-667-295-226

Sequence 2736, Ap
Sequence 2804, Ap
Sequence 2872, Ap
Sequence 3074, Ap
Sequence 69, Appl
Sequence 13950, A
Sequence 1347, Ap
Sequence 54, Appl
Sequence 274, App
Sequence 428, App
Sequence 17, Appl
Sequence 23874, A
Sequence 193, App
Sequence 7, Appli
Sequence 2881, Ap
Sequence 1646, Ap
Sequence 273, App
Sequence 1344, Ap
Sequence 5557, Ap
Sequence 170, App
Sequence 204, App
Sequence 3632, Ap
Sequence 6390, Ap
Sequence 2, Appli
Sequence 12351, A
Sequence 352, App
Sequence 8718, Ap
Sequence 8516, Ap
Sequence 144, App
Sequence 244, App
Sequence 24753, A
Sequence 230, App
Sequence 24752, A
Sequence 32959, A
Sequence 36, Appl
Sequence 579, App
Sequence 23873, A
Sequence 3856, Ap
Sequence 6602, Ap
Sequence 10256, A
Sequence 19, Appl
Sequence 546, App
Sequence 777, App
Sequence 804, App
Sequence 24751, A
Sequence 3999, Ap
Sequence 266, App
Sequence 207, App
Sequence 165, App
Sequence 580, App
Sequence 150, App
Sequence 230, App
Sequence 5188, Ap
Sequence 803, App
Sequence 802, App
Sequence 2823, Ap
Sequence 204, App
Sequence 23872, A
Sequence 2194, Ap
Sequence 9213, Ap
Sequence 1344, Ap
Sequence 2021, Ap
Sequence 167, App
Sequence 33021, A
Sequence 10737, A
Sequence 4302, Ap
Sequence 7429, Ap
Sequence 33958, A
Sequence 7, Appli
Sequence 10595, A
Sequence 3876, Ap
Sequence 33925, A


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; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-24

Query Match          100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 2 REDL 5

RESULT 4
US-11-045-024-4306
; Sequence 4306, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4306
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4306

Query Match          100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

US-11-045-024-4306
; Sequence 4306, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4306
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4306

Query Match          100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4
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Db 3 REDL 6

RESULT 5
US-11-045-024-9685
; Sequence 9685, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9685
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9685

Query Match          100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 6
US-11-045-024-12706
; Sequence 12706, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12706
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12706

Query Match          100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6
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; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12706
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
;
US-11-045-024-12706

Query Match      100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      3 REDL 6

RESULT 7
US-10-892-870-3
; Sequence 3, Application US/10892870
; Publication No. US20060014210A1
; GENERAL INFORMATION:
; APPLICANT: Agilent Technologies
; APPLICANT: Boyes, Barry E.
; APPLICANT: Liu, Hongbin E.
; APPLICANT: Nicol, Gordon R.
; TITLE OF INVENTION: Serial Derivatization of Peptides for De Novo Sequencing Using
; FILE REFERENCE: 10040405 KTM7374
; CURRENT APPLICATION NUMBER: US/10/892,870
; CURRENT FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: bovine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: peptide from cytochrome C (bovine heart)
US-10-892-870-3

Query Match      100.0%; Score 20; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      3 REDL 6

RESULT 8
US-10-938-690-3
; Sequence 3, Application US/10938690
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; Publication No. US20060014293A1
; GENERAL INFORMATION:
; APPLICANT: Agilent Technologies
; APPLICANT: Joyce, Timothy H.
; APPLICANT: Boyes, Barry E.
; APPLICANT: Nicol, Gordon R.
; APPLICANT: Liu, Hongbin
; TITLE OF INVENTION: Lock Mass Ions For Use With Derivatized Peptides for De Novo
; FILE REFERENCE: 10040464-1 KTM7374
; CURRENT APPLICATION NUMBER: US/10/938,690
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 10/892870
; PRIOR FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: bovine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: peptide from cytochrome C (bovine heart)
US-10-938-690-3

Query Match      100.0%; Score 20; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      3 REDL 6

RESULT 9
US-11-004-399-929
; Sequence 929, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 929
; LENGTH: 28
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-929

Query Match      100.0%; Score 20; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      6 REDL 9

RESULT 10
US-10-729-121-15
; Sequence 15, Application US/10729121
; Publication No. US20040144397A1
; GENERAL INFORMATION:
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; APPLICANT: Conkling, Mark
 ; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
 ; FILE REFERENCE: VTOB.033C1
 ; CURRENT APPLICATION NUMBER: US/10/729,121
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: 60/297,154
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: PCTUS02/18040
 ; PRIOR FILING DATE: 2002-06-06
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Salmonella typhimurium
 US-10-729-121-15

Query Match 100.0%; Score 20; DB 6; Length 37;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 5 REDL 8

RESULT 11

US-10-729-121-14
 ; Sequence 14, Application US/10729121
 ; Publication No. US20040144397A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conkling, Mark
 ; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
 ; FILE REFERENCE: VTOB.033C1
 ; CURRENT APPLICATION NUMBER: US/10/729,121
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: 60/297,154
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: PCTUS02/18040
 ; PRIOR FILING DATE: 2002-06-06
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum
 US-10-729-121-14

Query Match 100.0%; Score 20; DB 6; Length 38;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 5 REDL 8

RESULT 12

US-11-140-311-14
 ; Sequence 14, Application US/11140311
 ; Publication No. US20060035249A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ziermann, Rainer A.
 ; TITLE OF INVENTION: Means And Methods For Monitoring
 ; TITLE OF INVENTION: Protease Inhibitor Antiretroviral Therapy And Guiding
 ; FILE REFERENCE: 11068-154-999
 ; CURRENT APPLICATION NUMBER: US/11/140,311
 ; CURRENT FILING DATE: 2005-05-27
 ; PRIOR APPLICATION NUMBER: 09/874,472

; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: 09/766,344
 ; PRIOR FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: 09/663,458
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: 09/591,899
 ; PRIOR FILING DATE: 2000-06-12
 ; PRIOR APPLICATION NUMBER: 60/140,483
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 55
 ; TYPE: PRT
 ; ORGANISM: Human
 US-11-140-311-14

Query Match 100.0%; Score 20; DB 7; Length 55;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 3 REDL 6

RESULT 13

US-11-140-311-15
 ; Sequence 15, Application US/11140311
 ; Publication No. US20060035249A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Parkin, Neil T.
 ; APPLICANT: Ziermann, Rainer A.
 ; TITLE OF INVENTION: Means And Methods For Monitoring
 ; TITLE OF INVENTION: Protease Inhibitor Antiretroviral Therapy And Guiding
 ; FILE REFERENCE: 11068-154-999
 ; CURRENT APPLICATION NUMBER: US/11/140,311
 ; CURRENT FILING DATE: 2005-05-27
 ; PRIOR APPLICATION NUMBER: 09/874,472
 ; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: 09/766,344
 ; PRIOR FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: 09/663,458
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: 09/591,899
 ; PRIOR FILING DATE: 2000-06-12
 ; PRIOR APPLICATION NUMBER: 60/140,483
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 55
 ; TYPE: PRT
 ; ORGANISM: Human
 US-11-140-311-15

Query Match 100.0%; Score 20; DB 7; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 3 REDL 6

RESULT 14

US-10-475-075-913
 ; Sequence 913, Application US/10475075
 ; Publication No. US2006003498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bejanin, Stephanie
 ; APPLICANT: Tanaka, Hiroaki

APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
FILE REFERENCE: G-081US03PCT
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
SOFTWARE: Patent.pm
SEQ ID NO 913
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-10-475-075-913

Query Match 100.0%; Score 20; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 18 REDL 21

RESULT 15
US-10-934-944-148
Sequence 148, Application US/10934944
Publication No. US20060037096A1
GENERAL INFORMATION:
APPLICANT: Xu, Dongmei
TITLE OF INVENTION: Cloning of Cytochrome P450 Genes From Nicotiana
FILE REFERENCE: 07678/141008
CURRENT APPLICATION NUMBER: US/10/934,944
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 10/686,947
PRIOR FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/503,989
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 10/387,346
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: 10/340,861
PRIOR FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 10/293,252
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/418,933
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/363,684
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/347,444
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 60/337,684
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.3
SEQ ID NO 148
LENGTH: 61
TYPE: PRT
ORGANISM: Nicotiana tabacum
US-10-934-944-148

Query Match 100.0%; Score 20; DB 6; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 51 REDL 54

RESULT 16
US-11-116-881A-157
Sequence 157, Application US/11116881A
Publication No. US20060041949A1
GENERAL INFORMATION:
APPLICANT: Xu, Dongmei
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: 60/665,451
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/665,097
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/646,764
PRIOR FILING DATE: 2005-01-25
PRIOR APPLICATION NUMBER: 60/607,357
PRIOR FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/566,235
PRIOR FILING DATE: 2004-04-29
PRIOR APPLICATION NUMBER: 10/934,944
PRIOR FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 10/943,507
PRIOR FILING DATE: 2004-09-17
PRIOR APPLICATION NUMBER: 60/503,989
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/418,933
PRIOR FILING DATE: 2002-10-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2300
SOFTWARE: PatentIn version 3.3
SEQ ID NO 157
LENGTH: 61
TYPE: PRT
ORGANISM: Nicotiana tabacum
US-11-116-881A-157

Query Match 100.0%; Score 20; DB 7; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 51 REDL 54

RESULT 17
US-10-544-501-8
Sequence 8, Application US/10544501
Publication No. US20060037106A1
GENERAL INFORMATION:
APPLICANT: Cropdesign N.V.
TITLE OF INVENTION: Method for modifying plant growth characteristics
FILE REFERENCE: 4440-13
CURRENT APPLICATION NUMBER: US/10/544,501
CURRENT FILING DATE: 2005-08-04
PRIOR APPLICATION NUMBER: EP 03075363.6
PRIOR FILING DATE: 2003-02-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 72
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: peptidase_M24 domain of AtMAP2B
US-10-544-501-8

Query Match 100.0%; Score 20; DB 6; Length 72;

```
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 50 REDL 53

RESULT 18
US-11-096-568A-4959
; Sequence 4959, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4959
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(75)
; OTHER INFORMATION: Ceres Seq. ID no. 14306200
US-11-096-568A-4959

Query Match 100.0%; Score 20; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 69 REDL 72

RESULT 19
US-11-124-367A-275
; Sequence 275, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 275
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-275

Query Match 100.0%; Score 20; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 38 REDL 41

RESULT 20
US-11-124-367A-277
; Sequence 277, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-277

Query Match 100.0%; Score 20; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 38 REDL 41

RESULT 21
US-11-124-367A-278
; Sequence 278, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-278

Query Match 100.0%; Score 20; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 38 REDL 41

RESULT 22
US-11-124-367A-279
```

Mon Mar 20 08:51:25 2006

```
; Sequence 279, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-124-367A-279

Query Match      100.0%; Score 20; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      |||||
Db      38 REDL 41

RESULT 23
US-11-087-099-6823
; Sequence 6823, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6823
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Zea mays
; ORGANISM: Zea mays
US-11-087-099-6823

Query Match      100.0%; Score 20; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      |||||
Db      87 REDL 90

RESULT 24
US-10-793-626-2944
; Sequence 2944, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
US-10-793-626-2944
```

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; SEQ ID NO 2944
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2944

Query Match      100.0%; Score 20; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      |||||
Db      82 REDL 85

RESULT 25
US-10-667-295-226
; Sequence 226, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(112)
; OTHER INFORMATION: Ceres Seq. ID no. 13633592
US-10-667-295-226

Query Match      100.0%; Score 20; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      |||||
Db      17 REDL 20

RESULT 26
US-10-793-626-2796
; Sequence 2796, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2796
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2796
```

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Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 27
US-10-793-626-2804
; Sequence 2804, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2804
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2804

Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 28
US-10-793-626-2872
; Sequence 2872, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2872
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2872

Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 29
US-10-793-626-3074
; Sequence 3074, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3074
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3074

Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 30
US-11-098-686-69
; Sequence 69, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-69

Query Match      100.0%; Score 20; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      40 REDL 43

RESULT 31
US-11-096-568A-13950
; Sequence 13950, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
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Mon Mar 20 08:51:25 2006

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; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13950
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc.feature
; LOCATION: (1)-(122)
; OTHER INFORMATION: Ceres Seq. ID no. 15220798
US-11-096-568A-13950

Query Match      100.0%; Score 20; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      83 REDL 86

RESULT 32
US-11-051-720-1347
; Sequence 1347, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1347
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1347

Query Match      100.0%; Score 20; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      63 REDL 66

RESULT 33
US-11-019-711-54
; Sequence 54, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tchernov, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shionit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J

```

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; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Laminin B
; OTHER INFORMATION: Domain Consensus Sequence
US-11-019-711-54

Query Match      100.0%; Score 20; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      89 REDL 92

RESULT 34
US-11-124-367A-274
; Sequence 274, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274

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; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-274

Query Match      100.0%; Score 20; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      108 REDL 111
      |||||

RESULT 35
US-11-082-389-428
; Sequence 428, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 428
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-428

Query Match      100.0%; Score 20; DB 7; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      124 REDL 127
      |||||

RESULT 36
US-10-667-295-17
; Sequence 17, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
```

```
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12474811
US-10-667-295-17

Query Match      100.0%; Score 20; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      39 REDL 42
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RESULT 37
US-11-096-568A-23874
; Sequence 23874, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23874
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(141)
; OTHER INFORMATION: Ceres Seq. ID no. 12416018
US-11-096-568A-23874

Query Match      100.0%; Score 20; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      113 REDL 116
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RESULT 38
US-10-485-517-193
; Sequence 193, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynex Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: E100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
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; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-193

Query Match      100.0%; Score 20; DB 6; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        |||||
Db      137 REDL 140

RESULT 39
US-11-118-855-7
; Sequence 7, Application US/11118855
; Publication No. US20050266457A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Mohan
; TITLE OF INVENTION: Mutant Receptors and Their Use in a Nuclear Receptor-Based
; FILE OF INVENTION: Inducible Gene Expression System
; FILE REFERENCE: A01508-US
; CURRENT APPLICATION NUMBER: US/11/118,855
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US 60/567,294
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 60/609,424
; PRIOR FILING DATE: 2004-09-13
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-118-855-7

Query Match      100.0%; Score 20; DB 7; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        |||||
Db      74 REDL 77

RESULT 40
US-11-072-512-2881
; Sequence 2881, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI

; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US/11/072,512
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2881
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2881

Query Match      100.0%; Score 20; DB 7; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        |||||
Db      25 REDL 28

RESULT 41
US-10-821-234-1646
; Sequence 1646, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt_SEQ_genes version 1.0
; SEQ ID NO 1646
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1646

Query Match      100.0%; Score 20; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        |||||
Db      108 REDL 111

RESULT 42
US-11-124-367A-273
; Sequence 273, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO01519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
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; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 273
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-273

Query Match 100.0%; Score 20; DB 7; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 108 REDL 111

RESULT 43

US-10-821-234-1344
; Sequence 1344, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1344
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1344

Query Match 100.0%; Score 20; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 74 REDL 77

RESULT 44

US-11-087-099-5557
; Sequence 5557, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5557
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-087-099-5557

Query Match 100.0%; Score 20; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 105 REDL 108

RESULT 45

US-10-467-657-170
; Sequence 170, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 170
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-170

Query Match 100.0%; Score 20; DB 6; Length 164;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 62 REDL 65

RESULT 46

US-10-467-657-204
; Sequence 204, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 204
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-204

Query Match 100.0%; Score 20; DB 6; Length 164;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 62 REDL 65

RESULT 47

; TITLE OF INVENTION: Nucleic Acids, and Methods of Use

; FILE REFERENCE: P-LJ 5144
; CURRENT APPLICATION NUMBER: US/10/057,813
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/770,219
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-813-2

Query Match 100.0%; Score 20; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 163 REDL 166

RESULT 50

US-11-096-568A-12351
; Sequence 12351, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: Therby
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12351
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(168)
; OTHER INFORMATION: Ceres Seq. ID no. 13664315
US-11-096-568A-12351

Query Match 100.0%; Score 20; DB 7; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 28 REDL 31

Search completed: March 20, 2006, 07:53:54
Job time : 8.5 secs

US-10-467-657-3632
; Sequence 3632, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3632
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3632

Query Match 100.0%; Score 20; DB 6; Length 164;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 62 REDL 65

RESULT 48

US-10-467-657-6390
; Sequence 6390, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6390
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6390

Query Match 100.0%; Score 20; DB 6; Length 164;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 62 REDL 65

RESULT 49

US-10-057-813-2
; Sequence 2, Application US/10057813
; Publication No. US20060035359A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Okada, Kazuya
; TITLE OF INVENTION: Survivin-Binding Proteins, Encoding

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:41 ; Search time 401.5 Seconds
(without alignments)
13.768 Million cell updates/sec

Title: US-09-673-707-10
Perfect score: 20
Sequence: 1 REDL 4

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Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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51: /cgn2_6/ptodata/1/paa/US607 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	4	1	PCT-US03-18373-31	Sequence 31, Appl
3	20	100.0	4	1	PCT-US03-18373A-31	Sequence 31, Appl
4	20	100.0	4	1	PCT-US03-38227-12	Sequence 12, Appl
5	20	100.0	4	1	PCT-US03-39476-6	Sequence 6, Appli
6	20	100.0	4	1	PCT-US98-05710-11	Sequence 11, Appl
7	20	100.0	4	9	US-07-992-900A-4	Sequence 4, Appli
8	20	100.0	4	9	US-07-992-900A-4	Sequence 4, Appli
9	20	100.0	4	13	US-08-331-396A-52	Sequence 52, Appl
10	20	100.0	4	13	US-08-331-396C-52	Sequence 52, Appl
11	20	100.0	4	13	US-08-331-396D-52	Sequence 52, Appl
12	20	100.0	4	21	US-09-153-803-3	Sequence 3, Appli
13	20	100.0	4	22	US-09-250-056B-6	Sequence 6, Appli
14	20	100.0	4	24	US-09-410-362F-79	Sequence 79, Appl
15	20	100.0	4	24	US-09-462-682-12	Sequence 12, Appl
16	20	100.0	4	24	US-09-462-713-12	Sequence 12, Appl
17	20	100.0	4	24	US-09-480-236-7	Sequence 7, Appli
18	20	100.0	4	26	US-09-673-707-10	Sequence 10, Appl
19	20	100.0	4	26	US-09-684-599A-5	Sequence 5, Appli
20	20	100.0	4	27	US-09-743-173-1	Sequence 1, Appli
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22	20	100.0	4	29	US-09-979-539-7	Sequence 7, Appli
23	20	100.0	4	30	US-10-092-640-27	Sequence 27, Appl
24	20	100.0	4	31	US-10-112-788-16	Sequence 16, Appl
25	20	100.0	4	31	US-10-130-393-10	Sequence 10, Appl
26	20	100.0	4	32	US-10-297-337-16	Sequence 16, Appl
27	20	100.0	4	33	US-10-363-233-7	Sequence 7, Appli
28	20	100.0	4	34	US-10-406-830-24	Sequence 24, Appl
29	20	100.0	4	34	US-10-432-412-22	Sequence 22, Appl
30	20	100.0	4	34	US-10-432-412-23	Sequence 23, Appl
31	20	100.0	4	34	US-10-490-535-6	Sequence 6, Appli
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48	20	100.0	5	13	US-08-331-396C-53	Sequence 53, Appl
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53	20	100.0	5	22	US-09-247-139-37	Sequence 37, Appl
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55	20	100.0	5	24	US-09-410-362F-78	Sequence 78, Appl

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57	20	100.0	5	24	US-09-462-713-11	Sequence 11, Appl	130	20	100.0	11	39	US-10-938-690-3	Sequence 3, Appl
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59	20	100.0	5	26	US-09-673-707-11	Sequence 11, Appl	132	20	100.0	14	1	PCT-US98-23061-8	Sequence 8, Appl
60	20	100.0	5	26	US-09-684-599A-4	Sequence 4, Appl	133	20	100.0	14	1	PCT-US98-23061A-8	Sequence 8, Appl
61	20	100.0	5	29	US-09-979-539-8	Sequence 8, Appl	134	20	100.0	14	14	US-08-433-613-7	Sequence 7, Appl
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66	20	100.0	5	32	US-10-297-337-15	Sequence 15, Appl	139	20	100.0	15	27	US-09-786-635A-53	Sequence 53, Appl
67	20	100.0	5	34	US-10-406-830-23	Sequence 23, Appl	140	20	100.0	15	27	US-09-786-635C-53	Sequence 53, Appl
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95	20	100.0	8	40	US-11-045-024-9685	Sequence 9685, Ap							
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128	20	100.0	11	31	US-10-125-452-29	Sequence 29, Appl							

RESULT 1

PCT-US02-30316-6

Sequence 6, Application PC/TUS0230316

GENERAL INFORMATION:

APPLICANT: Pastan, Ira H.

APPLICANT: Beers, Richard

APPLICANT: Kreitman, Robert J.

APPLICANT: The Government of the United States of America

APPLICANT: as represented by The Secretary of the

Department of Health and Human Services

APPLICANT: Mutated Anti-CD22 Antibodies With Increased Affinity to

CD22-Expressing Leukemia Cells

TITLE OF INVENTION: CD22-Expressing Leukemia Cells

FILE REFERENCE: 015280-438100PC

CURRENT APPLICATION NUMBER: PCT/US02/30316

CURRENT FILING DATE: 2003-06-25

PRIOR APPLICATION NUMBER: US 60/325,360

PRIOR FILING DATE: 2001-09-26

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

TYPE: PRT

LENGTH: 4

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:carboxyl

OTHER INFORMATION: terminus addition to maintain ability of the

OTHER INFORMATION: construct to translocate to cytosol

PCT-US02-30316-6

Query Match 100.0%; Score 20; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 7.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 1 REDL 4

|||||

RESULT 2

PCT-US03-18373-31

Sequence 31, Application PC/TUS0318373

GENERAL INFORMATION:

APPLICANT: Pastan, Ira H.

APPLICANT: Nagata, Satoshi

APPLICANT: Onda, Masanori

PCT-US03-18373-31

```
; APPLICANT: Numata, Yoshito
; APPLICANT: Santora, Kenneth
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert
; APPLICANT: Sinha, Abhishek
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for
; TITLE OF INVENTION: Use in Immunotoxins
; FILE REFERENCE: 015280-464100PC
; CURRENT APPLICATION NUMBER: PCT/US03/18373
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 60/387,293
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/411,032
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas
; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition
PCT-US03-18373-31

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 3
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; Sequence 31, Application PC/TUS0318373A
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Nagata, Satoshi
; APPLICANT: Onda, Masanori
; APPLICANT: Numata, Yoshito
; APPLICANT: Santora, Kenneth
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert
; APPLICANT: Sinha, Abhishek
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for
; TITLE OF INVENTION: Use in Immunotoxins
; FILE REFERENCE: 015280-464100PC
; CURRENT APPLICATION NUMBER: PCT/US03/18373A
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 60/387,293
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/411,032
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas
; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition
PCT-US03-18373A-31

Query Match          100.0%; Score 20; DB 1; Length 4;
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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 4
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; Sequence 12, Application PC/TUS0338227
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
; TITLE OF INVENTION: (FV)-PE38 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLAST
; FILE REFERENCE: 4239-67287
; CURRENT APPLICATION NUMBER: PCT/US03/38227
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
PCT-US03-38227-12

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 5
PCT-US03-39476-6
; Sequence 6, Application PC/TUS0339476
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Eglund, Kristi A.
; APPLICANT: Vincent, James J.
; APPLICANT: Lee, Byungkook
; APPLICANT: Strausberg, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: BASE, a New Cancer Gene, and Uses Thereof
; FILE REFERENCE: 015280-475100PC
; CURRENT APPLICATION NUMBER: PCT/US03/39476
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,531
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:carboxyl
; OTHER INFORMATION: terminus addition sequence
PCT-US03-39476-6

Query Match          100.0%; Score 20; DB 1; Length 4;
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Mon Mar 20 08:51:25 2006

u8-09-673-707-10.ram

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
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IDb      1 REDL 4

RESULT 6
PCT-US98-05710-11
; Sequence 11, Application PC/TUS9805710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; TITLE OF INVENTION: CELL MEMBRANES
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/05710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,056
; FILING DATE: 26-MAR-1997
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US98-05710-11

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
       ||||
IDb      1 REDL 4

RESULT 7
US-07-992-900-4
; Sequence 4, Application US/07992900
; GENERAL INFORMATION:
; APPLICANT: DRAPER, ROCKFORD K.
; APPLICANT: CHAUDRY, G. JILANI
; TITLE OF INVENTION: POTENT AND SPECIFIC CHEMICALLY-CONJUGATED
; TITLE OF INVENTION: IMMUNOTOXINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/992,900
; FILING DATE: 19921216
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.

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; Sequence 52, Application US/08331396A
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira H.
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: TUMOR-SPECIFIC ANTIBODY FRAGMENTS,
; TITLE OF INVENTION: FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396A-52

Query Match 100.0%; Score 20; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 10
US-08-331-396C-52
; Sequence 52, Application US/08331396C
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

```
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396C
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396C-52

Query Match 100.0%; Score 20; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 11
US-08-331-396D-52
; Sequence 52, Application US/08331396D
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody
; TITLE OF INVENTION: Fragments, Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396D
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
```

```

; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: 12-OCT-1990
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-396D-52

```

```

Query Match      100.0%; Score 20; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 12
US-09-153-803-3
; Sequence 3, Application US/09153803
; GENERAL INFORMATION:
; APPLICANT: WEICHELBAUM, RALPH R.
; APPLICANT: SEETHARAM, SARA
; APPLICANT: KUFE, DONALD W.
; APPLICANT: PASTAN, IRA
; TITLE OF INVENTION: COMBINATION OF CHIMERIC EXOTOXIN AND THERAPEUTIC
; TITLE OF INVENTION: RADIATION
; FILE REFERENCE: ARSB:514
; CURRENT APPLICATION NUMBER: US/09/153,803
; CURRENT FILING DATE: 1998-09-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-153-803-3

```

```

Query Match      100.0%; Score 20; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 13
US-09-250-056B-6
; Sequence 6, Application US/09250056B
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Foul, Marie A
; TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
; FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Ab
; CURRENT APPLICATION NUMBER: US/09/250,056B
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/082,953

```

```

; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:: translocation
; OTHER INFORMATION: sequence
US-09-250-056B-6

```

```

Query Match      100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 14
US-09-410-362F-79
; Sequence 79, Application US/09410362F
; GENERAL INFORMATION:
; APPLICANT: CRAIK, CHARLES S.
; APPLICANT: TAKEUCHI, TOSHIHIKO
; APPLICANT: SCHUMAN, MARC
; TITLE OF INVENTION: MEMBRANE TYPE SERINE PROTEASE 1 (MT-SP1) AND USES THEREOF
; FILE REFERENCE: 28644-701.201
; CURRENT APPLICATION NUMBER: US/09/410,362F
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Endoplasmic refention sequence
US-09-410-362F-79

```

```

Query Match      100.0%; Score 20; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 15
US-09-462-682-12
; Sequence 12, Application US/09462682
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary,
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
; FILE REFERENCE: 015280-310100US
; CURRENT APPLICATION NUMBER: US/09/462,682
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/052,375
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14341
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-09-462-682-12

Query Match          100.0%; Score 20; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 16
US-09-462-713-12
; Sequence 12, Application US/09462713
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Mrsny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
; TITLE OF INVENTION: for Eliciting a Secretory IgA-Mediated Immune Response
; FILE REFERENCE: 015280-361100US
; CURRENT APPLICATION NUMBER: US/09/462,713
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-09-462-713-12

Query Match          100.0%; Score 20; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 17
US-09-480-236-7
; Sequence 7, Application US/09480236
; GENERAL INFORMATION:
; APPLICANT: Digan, Mary Ellen
; APPLICANT: Lake, Philip
; APPLICANT: Wright, Richard M.
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
; FILE REFERENCE: CGC 4-31157A/USN
; CURRENT APPLICATION NUMBER: US/09/480,236
; CURRENT FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PE peptide
US-09-480-236-7

Query Match          100.0%; Score 20; DB 24; Length 4;
```

```
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 18
US-09-673-707-10
; Sequence 10, Application US/09673707
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Bera, Tapan K.
; APPLICANT: Kennedy, Paul E.
; APPLICANT: Berger, Edward A.
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Immunotoxin Directed Against the HIV-1
; TITLE OF INVENTION: gp120 Envelope Glycoprotein
; FILE REFERENCE: 015280-356100US
; CURRENT APPLICATION NUMBER: US/09/673,707
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: WO PCT/US99/12909
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: US 60/088,860
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: carboxy
; OTHER INFORMATION: terminal sequence of Pseudomonas exotoxin (PE)
; OTHER INFORMATION: endoplasmic retention sequence
US-09-673-707-10

Query Match          100.0%; Score 20; DB 26; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 19
US-09-684-599A-5
; Sequence 5, Application US/09684599A
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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Mon Mar 20 08:51:25 2006

us-09-673-707-10.rapm

; APPLICATION NUMBER: US/09/684,599A
; FILING DATE: 05-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/215,035
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-259110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-684-599A-5

Query Match 100.0%; Score 20; DB 26; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|
|
|
|
DB 1 REDL 4

RESULT 20
US-09-743-173-1
; Sequence 1, Application US/09743173
; GENERAL INFORMATION:
; APPLICANT: Seveso, Michael
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Page, David T.
; TITLE OF INVENTION: Enhanced Delivery of Nucleic Acid-Based Drugs
; FILE REFERENCE: P24,376-A USA
; CURRENT APPLICATION NUMBER: US/09/743,173
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: PCT/GB00/01726
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,603
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: endosome escape motif
US-09-743-173-1

Query Match 100.0%; Score 20; DB 27; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|
|
|
|
DB 1 REDL 4

RESULT 21
US-09-763-393-15
; Sequence 15, Application US/09763393

; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Pastan, Ira
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Vasmatazis, George
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: PAGE-4, an X-Linked GAGE-Like Gene Expressed in Normal and
; TITLE OF INVENTION: Neoplastic Prostate, Testis and Uterus, and Uses Therefor
; FILE REFERENCE: 4239-61541-01
; CURRENT APPLICATION NUMBER: US/09/763,393
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: PCT/US99/20046
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 60/098,993
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Carboxyl terminus
US-09-763-393-15

Query Match 100.0%; Score 20; DB 27; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|
|
|
|
DB 1 REDL 4

RESULT 22
US-09-979-539-7
; Sequence 7, Application US/09979539
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chowdhury, Partha S.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity
; FILE REFERENCE: 015280-395100US
; CURRENT APPLICATION NUMBER: US/09/979,539
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US 60/160,071
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: WO PCT/US00/14829
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: addition at carboxyl terminus to maintain ability
; OTHER INFORMATION: to translocate into the cytosol
US-09-979-539-7

Query Match 100.0%; Score 20; DB 29; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|
|
|
|
DB 1 REDL 4

RESULT 23
US-10-092-640-27
; Sequence 27, Application US/10092640
; GENERAL INFORMATION:
; APPLICANT: Markle, James D.
; TITLE OF INVENTION: Novel High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quine Intellectual Property Law Group P.C.
; STREET: 2033 Clement Ave. Suite 200
; CITY: Alameda
; STATE: California
; COUNTRY: USA
; ZIP: 94501
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/092,640
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; APPLICATION NUMBER: US 09/315,574
; FILING DATE: 20-MAY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-092-640-27

Query Match 100.0%; Score 20; DB 30; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 24
US-10-112-788-16
; Sequence 16, Application US/10112788
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY
; APPLICANT: WINTHROP, MICHELLE
; APPLICANT: DENARDO, GERALD
; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
; FILE REFERENCE: 309T-000210US
; CURRENT APPLICATION NUMBER: US/10/112,788
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,721

; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant translocation peptide
US-10-112-788-16

Query Match 100.0%; Score 20; DB 31; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 25
US-10-130-393-10
; Sequence 10, Application US/10130393
; GENERAL INFORMATION:
; APPLICANT: Puri, Raj K.
; APPLICANT: Oshima, Yasuo
; APPLICANT: Joshi, Bharat H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; Department of Health and Human Services
; TITLE OF INVENTION: Modulating IL-13 Activity Using Mutated IL-13 Molecules
; TITLE OF INVENTION: That Are Antagonists or Agonists of IL-13
; FILE REFERENCE: 015280-409100US
; CURRENT APPLICATION NUMBER: US/10/130,393
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/165,236
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: WO PCT/US00/31044
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; LENGTH: 4
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: retention sequence
US-10-130-393-10

Query Match 100.0%; Score 20; DB 31; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 26
US-10-297-337-16
; Sequence 16, Application US/10297337
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Teutsami, Yasuo
; APPLICANT: Onda, Masanori
; APPLICANT: Nagata, Satoshi
; APPLICANT: Lee, Byungkook
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; Department of Health and Human Services
; TITLE OF INVENTION: PEGylation of Linkers Improves Antitumor Activity and

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; TITLE OF INVENTION: Reduces Toxicity of Immunoconjugates
; FILE REFERENCE: 015280-423200US
; CURRENT APPLICATION NUMBER: US/10/297,337
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/211,331
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/213,804
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: WO PCT/US01/18503
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal
; OTHER INFORMATION: variation to maintain ability of construct to
; OTHER INFORMATION: translocate to cytosol
US-10-297-337-16

```

```

Query Match 100.0%; Score 20; DB 32; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 REDL 4
Db 1 REDL 4

```

```

RESULT 27
US-10-363-233-7
; Sequence 7, Application US/10363233
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Liu, Xiu Fen
; APPLICANT: Bera, Tapan K.
; APPLICANT: Lee, Byungkook
; APPLICANT: Eglund, Kristi A.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: XAGE-1, a Gene Expressed in Multiple Cancers, and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 015280-420100US
; CURRENT APPLICATION NUMBER: US/10/363,233
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/229,684
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: WO PCT/US01/27258
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas
; OTHER INFORMATION: exotoxin carboxy terminus addition
US-10-363-233-7

```

```

Query Match 100.0%; Score 20; DB 33; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 REDL 4
Db 1 REDL 4

```

RESULT 28

```

US-10-406-830-24
; Sequence 24, Application US/10406830
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN FV ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Translocation signaling sequence.
US-10-406-830-24

```

```

Query Match 100.0%; Score 20; DB 34; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 REDL 4
Db 1 REDL 4

```

```

RESULT 29
US-10-432-412-22
; Sequence 22, Application US/10432412
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain
US-10-432-412-22

```

```

Query Match 100.0%; Score 20; DB 34; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 REDL 4
Db 1 REDL 4

```

```

RESULT 30
US-10-432-412-23
; Sequence 23, Application US/10432412

```

; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain
US-10-432-412-23

Query Match 100.0%; Score 20; DB 34; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 31
US-10-490-535-6
; Sequence 6, Application US/10490535
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Salvatore, Giuliana
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100US
; CURRENT APPLICATION NUMBER: US/10/490,535
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: WO PCT/US02/30316
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: carboxyl
; OTHER INFORMATION: terminus addition to maintain ability of the
; OTHER INFORMATION: construct to translocate to cytosol
US-10-490-535-6

Query Match 100.0%; Score 20; DB 34; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 32
US-10-537-061-12
; Sequence 12, Application US/10537061
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
; FILE REFERENCE: 4239-67287-05
; CURRENT APPLICATION NUMBER: US/10/537,061
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: PCT/US03/038227
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-537-061-12

Query Match 100.0%; Score 20; DB 35; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 33
US-10-659-036-12
; Sequence 12, Application US/10659036
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: Mrsn, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for
; TITLE OF INVENTION: Eliciting a Secretory IgA-Mediated Immune Response
; FILE REFERENCE: 015280-361200US
; CURRENT APPLICATION NUMBER: US/10/659,036
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 09/462,713
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-10-659-036-12

Query Match 100.0%; Score 20; DB 36; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 REDL 4 		
Db	1 REDL 4		
RESULT 34			
US-10-973-718-9			
; Sequence 9, Application US/10973718			
; GENERAL INFORMATION:			
; APPLICANT: Pastan, Ira H.			
; APPLICANT: Chowdhury, Partha S.			
; APPLICANT: The Government of the United States			
; APPLICANT: as represented by The Secretary of the			
; APPLICANT: Department of Health and Human Services			
; TITLE OF INVENTION: Antibodies, including Fv molecules, and			
; TITLE OF INVENTION: Immunocjugates Having High Binding Affinity for			
; TITLE OF INVENTION: Mesothelin and Methods for Their Use			
; FILE REFERENCE: 015280-339100US			
; CURRENT APPLICATION NUMBER: US/10/973,718			
; CURRENT FILING DATE: 2004-10-25			
; PRIOR APPLICATION NUMBER: US/09/581,345			
; PRIOR FILING DATE: 2000-09-27			
; PRIOR APPLICATION NUMBER: US 60/067,175			
; PRIOR FILING DATE: 1997-12-01			
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270			
; PRIOR FILING DATE: 1998-11-25			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 9			
; LENGTH: 4			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence:carboxyl			
; OTHER INFORMATION: terminus			
US-10-973-718-9			
Query Match 100.0%; Score 20; DB 39; Length 4;			
Best Local Similarity 100.0%; Pred. No. 7.2e+06;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 REDL 4 		
Db	1 REDL 4		
RESULT 35			
US-11-019-027-16			
; Sequence 16, Application US/11019027			
; GENERAL INFORMATION:			
; APPLICANT: YAN, Wei			
; APPLICANT: SHEN, Wenyang			
; APPLICANT: ZHOU, Hongxing			
; APPLICANT: ZHOU, Chen			
; APPLICANT: COSMAN, David J.			
; APPLICANT: CARTER, Paul			
; APPLICANT: MARTIN, Francis H.			
; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES			
; FILE REFERENCE: A-890A			
; CURRENT APPLICATION NUMBER: US/11/019,027			
; CURRENT FILING DATE: 2004-12-21			
; PRIOR APPLICATION NUMBER: 60/605,902			
; PRIOR FILING DATE: 2004-08-31			
; PRIOR APPLICATION NUMBER: 60/531,714			
; PRIOR FILING DATE: 2003-12-22			
; NUMBER OF SEQ ID NOS: 73			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 16			
; LENGTH: 4			
; TYPE: PRT			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: ER localization signal			
US-11-019-027-16			
Query Match 100.0%; Score 20; DB 40; Length 4;			
Best Local Similarity 100.0%; Pred. No. 7.2e+06;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 REDL 4 		
Db	1 REDL 4		
RESULT 36			
US-11-021-438-19			
; Sequence 19, Application US/11021438			
; GENERAL INFORMATION:			
; APPLICANT: LIU, BIN			
; APPLICANT: MARKS, JAMES D.			
; TITLE OF INVENTION: PROSTATE CANCER SPECIFIC INTERNALIZING HUMAN ANTIBODIES			
; FILE REFERENCE: 407T-392710US			
; CURRENT APPLICATION NUMBER: US/11/021,438			
; CURRENT FILING DATE: 2004-12-21			
; PRIOR APPLICATION NUMBER: US 60/532,433			
; PRIOR FILING DATE: 2003-12-23			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 19			
; LENGTH: 4			
; TYPE: PRT			
; ORGANISM: Artificial			
; FEATURE:			
; OTHER INFORMATION: Peptide translocation signal sequence.			
US-11-021-438-19			
Query Match 100.0%; Score 20; DB 40; Length 4;			
Best Local Similarity 100.0%; Pred. No. 7.2e+06;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 REDL 4 		
Db	1 REDL 4		
RESULT 37			
US-11-253-869-79			
; Sequence 79, Application US/11253869			
; GENERAL INFORMATION:			
; APPLICANT: CRAIK, CHARLES S.			
; APPLICANT: TAKEUCHI, TOSHIHIKO			
; APPLICANT: SCHUMAN, MARC			
; TITLE OF INVENTION: MT-SP1 POLYNUCLEOTIDES AND POLYPEPTIDES			
; FILE REFERENCE: 28644-701.303			
; CURRENT APPLICATION NUMBER: US/11/253,869			
; CURRENT FILING DATE: 2005-10-18			
; NUMBER OF SEQ ID NOS: 83			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 79			
; LENGTH: 4			
; TYPE: PRT			
; ORGANISM: Artificial			
; FEATURE:			
; OTHER INFORMATION: Endoplasmic refention sequence			
US-11-253-869-79			
Query Match 100.0%; Score 20; DB 42; Length 4;			
Best Local Similarity 100.0%; Pred. No. 7.2e+06;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 REDL 4 		
Db	1 REDL 4		


```
RESULT 38
US-11-254-185-79
; Sequence 79, Application US/11254185
; GENERAL INFORMATION:
; APPLICANT: CRAIK, CHARLES S.
; APPLICANT: TAKEUCHI, TOSHIHIKO
; APPLICANT: SCHUMAN, MARC
; TITLE OF INVENTION: MT-SP1 SERINE PROTEASE
; FILE REFERENCE: 28644-701.302
; CURRENT APPLICATION NUMBER: US/11/254.185
; CURRENT FILING DATE: 2005-10-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Endoplasmic refention sequence
US-11-254-185-79
Query Match 100.0%; Score 20; DB 42; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 39
US-60-042-056-11
; Sequence 11, Application US/60042056
; GENERAL INFORMATION:
; APPLICANT: Draper, Rockford
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: USF:072P21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-60-042-056-11
Query Match 100.0%; Score 20; DB 44; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 40
PCT-US00-29080-5
; Sequence 5, Application PC/TUS0029080
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Mresny, Randall J.
; APPLICANT: McKee, Marian
; APPLICANT: Daugherty, Ann
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Delivery of Proteins Across Polar Epithelial Cell
; TITLE OF INVENTION: Layers
; FILE REFERENCE: 015280-378100PC
; CURRENT APPLICATION NUMBER: PCT/US00/29080
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,923
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum retention sequence
PCT-US00-29080-5
Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 41
PCT-US02-30316-7
; Sequence 7, Application PC/TUS0230316
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Salvatore, Giuliana
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100PC
; CURRENT APPLICATION NUMBER: PCT/US02/30316
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminal
; OTHER INFORMATION: native sequence
```

```

PCT-US02-30316-7
Query Match      100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      ||||
Db      1 REDL 4

RESULT 42
PCT-US03-10630-4
; Sequence 4, Application PC/TUS0310630
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015
; CURRENT APPLICATION NUMBER: PCT/US03/10630
; CURRENT FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US03-10630-4

Query Match      100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      ||||
Db      1 REDL 4

RESULT 43
PCT-US03-10630A-4
; Sequence 4, Application PC/TUS0310630A
; GENERAL INFORMATION:
; APPLICANT: Kimberly A. Kelly
; APPLICANT: David A. Jones
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015US1
; CURRENT APPLICATION NUMBER: PCT/US03/10630A
; CURRENT FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/US03/10630
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US03-10630A-4

Query Match      100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      ||||
Db      1 REDL 4

RESULT 44
PCT-US98-05710-10
; Sequence 10, Application PC/TUS9805710
; GENERAL INFORMATION:
; APPLICANT: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; TITLE OF INVENTION: CELL MEMBRANES
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/05710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,056
; FILING DATE: 26-MAR-1997
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US98-05710-10

Query Match      100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
      ||||
Db      1 REDL 4

RESULT 45
US-08-224-831-32
; Sequence 32, Application US/08224831
; GENERAL INFORMATION:
; APPLICANT: Morgan, Charles A.
; TITLE OF INVENTION: RECEPTOR MODULATING AGENTS AND METHODS
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,831
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 930063.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-224-831-32

```

Query Match 100.0%; Score 20; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 46

US-08-224-831A-32
; Sequence 32, Application US/08224831A
; GENERAL INFORMATION:
; APPLICANT: Morgan, A. Charles
; TITLE OF INVENTION: RECEPTOR MODULATING AGENTS AND METHODS
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224.831A
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 930063.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: linear
; US-08-224-831A-32

Query Match 100.0%; Score 20; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 47

US-08-331-396A-53
; Sequence 53, Application US/08331396A
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira H.
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: TUMOR-SPECIFIC ANTIBODY FRAGMENTS,
; TITLE OF INVENTION: FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Steuart Street Tower, One Market Plaza

CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.396A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396A-53

Query Match 100.0%; Score 20; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 48

US-08-331-396C-53
; Sequence 53, Application US/08331396C
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.396C
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396C-53

Query Match 100.0%; Score 20; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4

RESULT 50
US-09-153-803-2
; Sequence 2, Application US/09153803
; GENERAL INFORMATION:
; APPLICANT: WEICHSELBAUM, RALPH R.
; APPLICANT: SEETHARAM, SARA
; APPLICANT: KUFE, DONALD W.
; APPLICANT: PASTAN, IRA
; TITLE OF INVENTION: COMBINATION OF CHIMERIC EXOTOXIN AND THERAPEUTIC
; FILE REFERENCE: ARSB:514
; CURRENT APPLICATION NUMBER: US/09/153,803
; CURRENT FILING DATE: 1998-09-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
; US-09-153-803-2

Query Match 100.0%; Score 20; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4

Search completed: March 20, 2006, 08:10:49
Job time : 404.5 secs

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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:40 ; Search time 17.5 Seconds
(without alignments)
21.955 Million cell updates/sec

Title: US-09-673-707-10
Perfect score: 20
Sequence: 1 REDL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 443638 seqs, 96052105 residues

Total number of hits satisfying chosen parameters: 443638

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Pending_Patents_AA New:*
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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	6 US-11-055-181-5	Sequence 5, Appli
2	20	100.0	4	6 US-11-154-103-24	Sequence 24, Appli
3	20	100.0	4	6 US-10-432-412A-22	Sequence 22, Appli
4	20	100.0	5	6 US-11-055-181-4	Sequence 4, Appli
5	20	100.0	5	6 US-11-154-103-23	Sequence 23, Appli
6	20	100.0	5	6 US-11-344-466-7	Sequence 7, Appli
7	20	100.0	5	6 US-10-432-412A-21	Sequence 21, Appli
8	20	100.0	5	6 US-10-110-880-5	Sequence 5, Appli
9	20	100.0	6	8 US-60-772-986-4665	Sequence 4665, Ap
10	20	100.0	9	8 US-60-772-986-5174	Sequence 5174, Ap
11	20	100.0	10	4 US-08-838-916J-35	Sequence 35, Appli
12	20	100.0	15	6 US-10-560-069-794	Sequence 794, App
13	20	100.0	19	6 US-11-303-372-4	Sequence 4, Appli
14	20	100.0	19	6 US-11-303-372-62	Sequence 62, Appli
15	20	100.0	19	8 US-60-772-986-9495	Sequence 9495, Ap
16	20	100.0	19	8 US-60-772-986-12177	Sequence 12177, A
17	20	100.0	28	6 US-10-004-399A-929	Sequence 929, App
18	20	100.0	32	6 US-10-561-506-100	Sequence 100, App
19	20	100.0	37	6 US-11-285-537-15	Sequence 15, Appli
20	20	100.0	37	6 US-10-729-121-15	Sequence 15, Appli
21	20	100.0	37	8 US-60-734-556-19	Sequence 19, Appli
22	20	100.0	37	8 US-60-734-556-20	Sequence 20, Appli
23	20	100.0	38	6 US-11-285-537-14	Sequence 14, Appli
24	20	100.0	38	6 US-10-729-121-14	Sequence 14, Appli
25	20	100.0	46	8 US-60-734-556-23	Sequence 23, Appli

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Sequence 145914,
Sequence 738, App
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Sequence 6, Appli
Sequence 7, Appli
Sequence 126856,
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Sequence 13193, A
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Sequence 14945, A
Sequence 991, App
Sequence 162235,
Sequence 171301,
Sequence 12353,
Sequence 15402,
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Sequence 10208, A
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Sequence 23719, A
Sequence 26304, A
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99 20 100.0 145 7 US-11-360-355-168720 Sequence 168720, A
100 20 100.0 146 8 US-60-752-355-37244 Sequence 37244, A
101 20 100.0 147 5 US-09-965-703A-44 Sequence 44, Appl
102 20 100.0 147 6 US-10-561-829-156 Sequence 156, Appl
103 20 100.0 148 6 US-10-953-349-3244 Sequence 3244, Ap
104 20 100.0 148 7 US-11-360-355-151749 Sequence 151749, A
105 20 100.0 150 6 US-10-953-349-13032 Sequence 13032, A
106 20 100.0 150 6 US-10-953-349-22054 Sequence 22054, A
107 20 100.0 150 6 US-10-953-349-16002 Sequence 16002, A
108 20 100.0 150 8 US-60-752-355-51965 Sequence 51965, A
109 20 100.0 151 6 US-11-287-460-16 Sequence 16, Appl
110 20 100.0 151 6 US-10-200-148B-16 Sequence 16, Appl
111 20 100.0 151 8 US-60-658-984A-7590 Sequence 7590, Ap
112 20 100.0 152 6 US-10-567-867-281 Sequence 281, Appl
113 20 100.0 152 7 US-11-360-355-131210 Sequence 131210, A
114 20 100.0 152 8 US-60-742-219-1614 Sequence 1614, Ap
115 20 100.0 152 8 US-60-751-420-1506 Sequence 1506, Ap
116 20 100.0 153 6 US-11-287-460-22 Sequence 22, Appl
117 20 100.0 153 6 US-11-287-460-24 Sequence 24, Appl
118 20 100.0 153 6 US-11-287-460-28 Sequence 28, Appl
119 20 100.0 153 6 US-11-045-004-1606 Sequence 1606, Ap
120 20 100.0 153 6 US-10-200-148B-33 Sequence 33, Appl
121 20 100.0 153 6 US-10-200-148B-35 Sequence 35, Appl
122 20 100.0 153 6 US-10-200-148B-36 Sequence 36, Appl
123 20 100.0 153 6 US-10-461-673-13018 Sequence 13018, A
124 20 100.0 154 6 US-11-287-460-2 Sequence 2, Appl
125 20 100.0 154 6 US-11-287-460-21 Sequence 21, Appl
126 20 100.0 154 6 US-11-287-460-23 Sequence 23, Appl
127 20 100.0 154 6 US-11-347-750-107 Sequence 107, Appl
128 20 100.0 154 6 US-10-200-148B-2 Sequence 2, Appl
129 20 100.0 154 6 US-10-200-148B-32 Sequence 32, Appl
130 20 100.0 154 6 US-10-200-148B-34 Sequence 34, Appl
131 20 100.0 154 6 US-10-529-348-92 Sequence 92, Appl
132 20 100.0 154 6 US-10-529-348-1172 Sequence 1172, Ap
133 20 100.0 154 7 US-11-360-355-133627 Sequence 133627, A
134 20 100.0 154 7 US-11-360-355-163885 Sequence 163885, A
135 20 100.0 154 7 US-11-360-355-171136 Sequence 171136, A
136 20 100.0 155 7 US-11-360-355-166976 Sequence 166976, A
137 20 100.0 156 1 PCT-US06-00964-4820 Sequence 4820, Ap
138 20 100.0 156 6 US-11-330-403-4820 Sequence 4820, Ap
139 20 100.0 159 7 US-11-360-355-159530 Sequence 159530, A
140 20 100.0 160 8 US-60-658-984A-18730 Sequence 18730, A
141 20 100.0 161 6 US-11-293-697-4471 Sequence 4471, Ap
142 20 100.0 161 8 US-60-658-984A-13186 Sequence 13186, A
143 20 100.0 163 1 PCT-US06-00964-17630 Sequence 17630, A
144 20 100.0 163 6 US-11-330-403-17630 Sequence 17630, A
145 20 100.0 163 6 US-10-276-817B-14445 Sequence 14445, A
146 20 100.0 165 8 US-60-658-984A-19752 Sequence 19752, A
147 20 100.0 166 6 US-10-953-349-36001 Sequence 36001, A
148 20 100.0 166 7 US-11-360-355-153983 Sequence 153983, A
149 20 100.0 166 7 US-11-360-355-158374 Sequence 158374, A
150 20 100.0 167 6 US-10-953-349-35968 Sequence 35968, A

ALIGNMENTS

RESULT 1
US-11-055-181-5
; Sequence 5, Application US/11055181
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY J.
; APPLICANT: DENARDO, RODNEY
; APPLICANT: BALHORN, GERALD 1.
; TITLE OF INVENTION: SELECTIVE HIGH-AFFINITY POLYDENTATE LIGANDS AND METHODS OF MAKING
; FILE REFERENCE: 309T-3005100S
; CURRENT APPLICATION NUMBER: US/11/055,181
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,444
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic translocation signaling sequence.
US-11-055-181-5

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 2
US-11-154-103-24
; Sequence 24, Application US/11154103
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Translocation signaling sequence.
US-11-154-103-24

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 3
US-10-432-412A-22
; Sequence 22, Application US/10432412A
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412A
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain
US-10-432-412A-22

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 1 REDL 4

RESULT 4

US-11-055-181-4
; Sequence 4, Application US/11055181
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY J.
; APPLICANT: DENARDO, GERALD L.
; APPLICANT: BALHORN, RODNEY
; TITLE OF INVENTION: SELECTIVE HIGH-AFFINITY POLYDENTATE LIGANDS AND METHODS OF MAKING
; TITLE OF INVENTION: SUCH
; FILE REFERENCE: 309t-3005100US
; CURRENT APPLICATION NUMBER: US/11/055,181
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,444
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic translocation signaling sequence.
US-11-055-181-4

Query Match 100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 1 REDL 4

RESULT 5

US-11-154-103-23
; Sequence 23, Application US/11154103
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial

; FEATURE:
; OTHER INFORMATION: Translocation signaling sequence.
US-11-154-103-23

Query Match 100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 1 REDL 4

RESULT 6

US-11-344-466-7
; Sequence 7, Application US/11344466
; GENERAL INFORMATION:
; APPLICANT: Fey, Georg H
; APPLICANT: Peipp, Matthias
; APPLICANT: Schwemmlin, Michael
; TITLE OF INVENTION: CD19-Specific Immunotoxin and Treatment Method
; FILE REFERENCE: 59849-8005
; CURRENT APPLICATION NUMBER: US/11/344,466
; CURRENT FILING DATE: 2006-01-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic transport sequence
US-11-344-466-7

Query Match 100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 1 REDL 4

RESULT 7

US-10-432-412A-21
; Sequence 21, Application US/10432412A
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; TITLE OF INVENTION: Exotoxin A and type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412A
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain in native
; OTHER INFORMATION: Pseudomonas exotoxin A
US-10-432-412A-21

Query Match 100.0%; Score 20; DB 6; Length 5;

Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 REDL 4
 ||||
Db 1 REDL 4

RESULT 8
US-10-110-880-5
; Sequence 5, Application US/10110880
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Mzeny, Randall J.
; APPLICANT: McKee, Marian
; APPLICANT: Daugherty, Ann
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Delivery of Proteins Across Polar Epithelial Cell
; FILE REFERENCE: Layers
; FILE REFERENCE: 015280-378100US
; CURRENT APPLICATION NUMBER: US/10/110,880
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/160,923
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: WO PCT/US00/29080
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum retention sequence
US-10-110-880-5

Query Match 100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 REDL 4
 ||||
Db 1 REDL 4

RESULT 9
US-60-772-986-4665
; Sequence 4665, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; TITLE OF INVENTION: INTERACTION WITHIN HUMAN PROTEINS AND USSES THEREFOR
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4665
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-4665

Query Match 100.0%; Score 20; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 REDL 4

Db 2 REDL 5

RESULT 10
US-60-772-986-5174
; Sequence 5174, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; TITLE OF INVENTION: INTERACTION WITHIN HUMAN PROTEINS AND USES THEREFOR
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5174
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-5174

Query Match 100.0%; Score 20; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 REDL 4
 ||||
Db 4 REDL 7

RESULT 11
US-08-838-916J-35
; Sequence 35, Application US/08838916J
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Grassy, Gerald
; APPLICANT: Calas, Bernard
; TITLE OF INVENTION: Cytomodulating Lipophilic Peptides for Inhibiting Lymphocyte
; TITLE OF INVENTION: Activity
; FILE REFERENCE: A-64360
; CURRENT APPLICATION NUMBER: US/08/838,916J
; CURRENT FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-838-916J-35

Query Match 100.0%; Score 20; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 REDL 4
 ||||
Db 1 REDL 4

RESULT 12
US-10-560-069-794
; Sequence 794, Application US/10560069
; GENERAL INFORMATION:
; APPLICANT: KENT, Stephen J.
; TITLE OF INVENTION: Immunomodulating compositions, uses therefor and processes for
; TITLE OF INVENTION: production
; FILE REFERENCE: 21415-0021.01-US

; CURRENT APPLICATION NUMBER: US/10/560,069
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: PCT/AU2004/000775
; PRIOR FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 2003902875
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 2004901589
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 2232
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 794
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HIV-1 pol peptide 1
US-10-560-069-794

Query Match 100.0%; Score 20; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 3 REDL 6

RESULT 13

US-11-303-372-4

; Sequence 4, Application US/11303372
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-11-303-372-4

Query Match 100.0%; Score 20; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 16 REDL 19

RESULT 14

US-11-303-372-62

; Sequence 62, Application US/11303372
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.

; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(19)
; OTHER INFORMATION: D form amino acid
US-11-303-372-62

Query Match 100.0%; Score 20; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 16 REDL 19

RESULT 15

US-60-772-986-9495

; Sequence 9495, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Targuy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; TITLE OF INVENTION: INTERACTION WITHIN HUMAN PROTEINS AND USES THEREFOR
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9495
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-9495

Query Match 100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||
Db 15 REDL 18

RESULT 16

US-60-772-986-12177

; Sequence 12177, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith

```
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; TITLE OF INVENTION: INTERACTION WITHIN HUMAN PROTEINS AND USES THEREFOR
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12177
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-12177

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 6 REDL 9

RESULT 17
US-11-004-399A-929
; Sequence 929, Application US/11004399A
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399A
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 929
; LENGTH: 28
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399A-929

Query Match      100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 6 REDL 9

RESULT 18
US-10-561-506-100
; Sequence 100, Application US/10561506
; GENERAL INFORMATION:
; APPLICANT: MEINKE, ANDREAS
; APPLICANT: NAGY, ESZTER
; APPLICANT: WINKLER, BIRGIT
; TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENS
; FILE REFERENCE: SONN:085US
; CURRENT APPLICATION NUMBER: US/10/561,506
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: PCT/EP2004/006460
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: EP03450148.6
; PRIOR FILING DATE: 2003-06-17
```

```
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-561-506-100

Query Match      100.0%; Score 20; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 19
US-11-285-537-15
; Sequence 15, Application US/11285537
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; TITLE OF INVENTION: LEVELS IN TOBACCO
; FILE REFERENCE: VTOB.033C1C1
; CURRENT APPLICATION NUMBER: US/11/285,537
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: 11/077,752
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 10/729,121
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-11-285-537-15

Query Match      100.0%; Score 20; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 20
US-10-729-121-15
; Sequence 15, Application US/10729121
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; TITLE OF INVENTION: LEVELS IN TOBACCO
; FILE REFERENCE: VTOB.033C1
; CURRENT APPLICATION NUMBER: US/10/729,121
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 37
```

; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-729-121-15

Query Match 100.0%; Score 20; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 21

US-60-734-556-19
; Sequence 19, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-19

Query Match 100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 34 REDL 37

RESULT 22

US-60-734-556-20
; Sequence 20, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-20

Query Match 100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 34 REDL 37

RESULT 23

US-11-285-537-14
; Sequence 14, Application US/11285537
; GENERAL INFORMATION:

; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; TITLE OF INVENTION: LEVELS IN TOBACCO
; FILE REFERENCE: VTOB.033C1C1
; CURRENT APPLICATION NUMBER: US/11/285,537
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: 11/077,752
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 10/729,121
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-285-537-14

Query Match 100.0%; Score 20; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 24

US-10-729-121-14
; Sequence 14, Application US/10729121
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; TITLE OF INVENTION: LEVELS IN TOBACCO
; FILE REFERENCE: VTOB.033C1
; CURRENT APPLICATION NUMBER: US/10/729,121
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-729-121-14

Query Match 100.0%; Score 20; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 25

US-60-734-556-23
; Sequence 23, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08

```

; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 46
; TYPE: prt
; ORGANISM: Mus musculus
US-60-734-556-23

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```
Query Match      100.0%; Score 20; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1 REDL 4
D _b	43 REDL 46

RESULT 26
US-60-734-556-16
: Sequence 16. Application US/60734556

```

, GENERAL INFORMATION:
, APPLICANT: Bu, Guojun
, APPLICANT: Li, Yonghe
, TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
, TITLE OF INVENTION: Diseases and Methods Therefor
, FILE REFERENCE: 60005161-0190
, CURRENT APPLICATION NUMBER: US/60/734,556
, CURRENT FILING DATE: 2005-11-08
, NUMBER OF SEQ ID NOS: 32
, SOFTWARE: PatentIn version 3.3
, SEQ ID NO 16
, LENGTH: 47

```

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-734-556-16

Query Match	100.0%;	Score 20;	DB 8;	Length 47;
Best Local Similarity	100.0%;	Pred. No. 2.1e+02;		
Matches	4:	Conservative	0:	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy 1 REDL 4
44 REDL 47

RESULT 27
US-11-360-355-145914
: Sequence 145914. Application US/11360355

/ SEQUENCE INFORMATION:
 / GENERAL INFORMATION:
 / APPLICANT: Boukharov, Andrey
 / APPLICANT: Du, Zijing
 / APPLICANT: Guo, Liang
 / APPLICANT: Kovalic, David
 / APPLICANT: Lu, Maolong
 / APPLICANT: McCarter, James
 / APPLICANT: Miller, Nancy
 / APPLICANT: Williams, Deryck
 / APPLICANT: Vaudin, Mark
 / APPLICANT: Wu, Wei
 / TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
 / TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
 / FILE REFERENCE: 38-21(53885)
 / CURRENT APPLICATION NUMBER: US/11/360,355
 / CURRENT FILING DATE: 2006-02-24
 / NUMBER OF SEQ ID NOS: 171306
 / SEQ ID NO 145914

; LIFE: FRI
 ; ORGANISM: Heterodera glycines
 ; FEATURE:
 ; OTHER INFORMATION: Coding reg
 ; OTHER INFORMATION: -85,212-28
 US-11-360-355-145914

```

Query Match      100.0%; Score 20; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4: Conservative 0; Mismatches 0; Indels

```

Qy	1 REDL 4
Db	35 REDL 38

RESULT 28
US-60-732-162-738

Sequence 738, Application US/60732162

GENERAL INFORMATION:

APPLICANT: Belouchi, Abdelmajid

APPLICANT: Raelson, John V

APPLICANT: Bradley, Walter E

APPLICANT: Paquin, Bruno

APPLICANT: Fournier, Helene

APPLICANT: Nguyen-Huu, Quynh

APPLICANT: Croteau, Pascal

APPLICANT: Allard, Rene

APPLICANT: Debrus, Sophie

APPLICANT: Eerdewegh, Paul V

APPLICANT: Little, Randall D

APPLICANT: Keith, Tim

APPLICANT: Secal, Jonathan

APPLICANT: Segar, Jonathan
TITLE OF INVENTION: Genemap of the Human
FILE REFERENCE: 059908-5010-PR
CURRENT APPLICATION NUMBER: US/60/732,162

```

; CURRENT FILING DATE: 2005-11-02
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 738
; LENGTH: 51

```

ORGANISM: Homosapiens
UHS-60-732-162-738

Query Match 100.0%; Score 20; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels

Qy 1 REDL 4
|||
Db 16 REDL 19

RESULT 29
US-60-734-556-4
. Sequence 4. Application US/60734556

```

: sequence information: 0679000000
: GENERAL INFORMATION:
: APPLICANT: Bu, Guojun
: APPLICANT: Li, Yonghe
: TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
: TITLE OF INVENTION: Diseases and Methods Therefor
: FILE REFERENCE: 60005161-0190
: CURRENT APPLICATION NUMBER: US/60/734,556
: CURRENT FILING DATE: 2005-11-08
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 4
: LENGTH: 54
: TYPE: PRT
: ORGANISM: Mus musculus
: US-60-734-556-4

```

Query Match	100.0%;	Score 20;	DB 8;	Length 54;
Best Local Similarity	100.0%;	Pred. No. 2.5e+02;		
Matches	4:	Conservative	0:	Mismatches 0: Indels

Qy 1 REDL 4

```

; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_72337; Strand=+; Position=1
; OTHER INFORMATION: -85,213-281
US-11-360-355-145914

```

```
Db          51 REDL 54

RESULT 30
US-60-734-556-5
; Sequence 5, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; TITLE OF INVENTION: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-5

Query Match      100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      51 REDL 54

RESULT 31
US-60-734-556-8
; Sequence 8, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; TITLE OF INVENTION: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-60-734-556-8

Query Match      100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      51 REDL 54

RESULT 32
US-60-734-556-3
; Sequence 3, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; TITLE OF INVENTION: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3

Query Match      100.0%; Score 20; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      52 REDL 55

RESULT 33
US-60-734-556-6
; Sequence 6, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; TITLE OF INVENTION: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-60-734-556-6

Query Match      100.0%; Score 20; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      52 REDL 55

RESULT 34
US-60-734-556-7
; Sequence 7, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; TITLE OF INVENTION: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Pongo pygmaeus
US-60-734-556-7

Query Match      100.0%; Score 20; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      52 REDL 55

RESULT 35
US-11-360-355-126856
; Sequence 126856, Application US/11360355
```

```
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 126856
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_53279; Strand=-; Position=1
; OTHER INFORMATION: -16,232-431
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit_ID=NP_872170.1; Match level="QueryCoverage
; OTHER INFORMATION: =100%,HitCoverage=6%, E-value=4e-11, Identity=46%"; Hit descript
; OTHER INFORMATION: =ankyrim and patacin family member (5V188) [Caenorhabditis eleg
; OTHER INFORMATION: emb|CAD54162.1| Hypothetical protein W
US-11-360-355-126856

Query Match 100.0%; Score 20; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 REDL 4
Db 2 REDL 5

RESULT 36
US-11-360-355-149183
; Sequence 149183, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 149183
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_75606; Strand=-; Position=1
; OTHER INFORMATION: -85,643-773
US-11-360-355-149183

Query Match 100.0%; Score 20; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;
```

```
Qy 1 REDL 4
Db 15 REDL 18

RESULT 37
US-10-276-817B-11417
; Sequence 11417, Application US/10276817B
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: US/10/276,817B
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US01/14827
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 11417
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(72)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-276-817B-11417

Query Match 100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 REDL 4
Db 7 REDL 10

RESULT 38
US-10-953-349-28331
; Sequence 28331, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28331
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Triticum aestivum
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
US-10-953-349-28331

Query Match 100.0%; Score 20; DB 6; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 REDL 4
Db 59 REDL 62

RESULT 39
US-10-953-349-18313
; Sequence 18313, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28331
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Triticum aestivum
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
US-10-953-349-18313
```

; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18313
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18313

Query Match 100.0%; Score 20; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 69 REDL 72

RESULT 40
US-10-953-349-31993
; Sequence 31993, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31993
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31993

Query Match 100.0%; Score 20; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 23 REDL 26

RESULT 41
US-11-360-355-133143
; Sequence 133143, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 133143
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_59566; Strand=-; Position=1

; OTHER INFORMATION: -192,251-295
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=AAP80600.1; Match level="QueryCovera
; OTHER INFORMATION: =98%, HitCoverage=21%, E-value=3e-32, Identity=87%", Hit descri
; OTHER INFORMATION: =putative alpha-tubulin [Oikopleura dioica]
US-11-360-355-133143

Query Match 100.0%; Score 20; DB 7; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 52 REDL 55

RESULT 42
US-10-461-673-14945
; Sequence 14945, Application US/10461673
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Yonghong
; APPLICANT: Yang, Zhi Wei
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Wang, Dunrui
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Ujwal, Manusha L.
; APPLICANT: Ma, Yunqing
; APPLICANT: Chen, Rui-Hong
; APPLICANT: Ghosh, Malabika
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 823
; CURRENT APPLICATION NUMBER: US/10/461,673
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: PCT/US02/29964
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/245,014
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: PCT/US02/29636
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 10/245,817
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US02/29001
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 10/243,552
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US02/25485
; PRIOR FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 17116
; SOFTWARE: dc FL_genes Version 6.0
; SEQ ID NO 14945
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens

```
US-10-461-673-14945
Query Match      100.0%; Score 20; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 60 REDL 63
|||||

RESULT 43
US-10-498-451-991
; Sequence 991, Application US/10498451
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Ghosh, Malabika
; APPLICANT: Xue, Aidong J.
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Dunrui
; APPLICANT: Goodrich, Kyle W.
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wehrman, Tom
; APPLICANT: Weng, Gezhi
; APPLICANT: Xu, Chongjun
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 820/PCT
; CURRENT APPLICATION NUMBER: US/10/498,451
; CURRENT FILING DATE: 2004-05-09
; PRIOR APPLICATION NUMBER: US 60/339,739
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 10/128,558
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/365,384
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 60/365,091
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 60/372,615
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/376,045
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/372,381
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3134
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 991
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-498-451-991

Query Match      100.0%; Score 20; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
```

```
Db 60 REDL 63
|||||

RESULT 44
US-11-360-355-162235
; Sequence 162235, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 162235
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_88658; Strand=+; Position=3
US-11-360-355-162235

Query Match      100.0%; Score 20; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 49 REDL 52
|||||

RESULT 45
US-11-360-355-171301
; Sequence 171301, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 171301
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_97724; Strand=+; Position=3
US-11-360-355-171301

Query Match      100.0%; Score 20; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Qy 1 REDL 4
Db 49 REDL 52

RESULT 46

US-11-360-355-123353
; Sequence 123353, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 123353
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (60)..(60)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=AAC24580.1; Match level="QueryCoverage
; OTHER INFORMATION: =96%, HitCoverage=53%, E-value=8e-24, Identity=65%", Hit descrip
; OTHER INFORMATION: =ADP/ATP translocase [Heterodera glycines]
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Biological process=embryogenesis and morphogenesis
; FEATURE:
; OTHER INFORMATION: Essential gene: C elegans homolog=T27B9.1a; Phenotype=Emb
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_49776; Strand=+; Position=2-
US-11-360-355-123353

Query Match 100.0%; Score 20; DB 7; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 70 REDL 73

RESULT 47

US-11-360-355-158402
; Sequence 158402, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS

; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 158402
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_84825; Strand=-; Position=1
; OTHER INFORMATION: -156,213-323
US-11-360-355-158402

Query Match 100.0%; Score 20; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 47 REDL 50

RESULT 48

US-11-360-355-150094
; Sequence 150094, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 150094
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_76517; Strand=-; Position=1
; OTHER INFORMATION: -112,479-636
US-11-360-355-150094

Query Match 100.0%; Score 20; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 6 REDL 9

RESULT 49

US-10-461-673-10208
; Sequence 10208, Application US/10461673
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.

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; APPLICANT:  Xue, Aidong
; APPLICANT:  Wehrman, Tom
; APPLICANT:  Wang, Zhi Wei
; APPLICANT:  Yang, Yonghong
; APPLICANT:  Goodrich, Ryle W.
; APPLICANT:  Wang, Dunrui
; APPLICANT:  Yamazaki, Victoria
; APPLICANT:  Ujwal, Manusha L.
; APPLICANT:  Ma, Yunding
; APPLICANT:  Chen, Rui-Hong
; APPLICANT:  Ghosh, Malabika
; APPLICANT:  Weng, Gezhi
; APPLICANT:  Haley-Vicente, Dana
; APPLICANT:  Dmanac, Radoje T.
; TITLE OF INVENTION:  Novel Nucleic Acids and Polypeptides
; FILE REFERENCE:  823
; CURRENT APPLICATION NUMBER:  US/10/461,673
; CURRENT FILING DATE:  2003-06-13
; PRIOR APPLICATION NUMBER:  PCT/US02/29964
; PRIOR FILING DATE:  2002-09-19
; PRIOR APPLICATION NUMBER:  US 10/245,014
; PRIOR FILING DATE:  2002-09-16
; PRIOR APPLICATION NUMBER:  US 60/323,739
; PRIOR FILING DATE:  2001-09-19
; PRIOR APPLICATION NUMBER:  PCT/US02/29636
; PRIOR FILING DATE:  2002-09-18
; PRIOR APPLICATION NUMBER:  US 10/245,817
; PRIOR FILING DATE:  2002-09-16
; PRIOR APPLICATION NUMBER:  US 60/323,349
; PRIOR FILING DATE:  2001-09-18
; PRIOR APPLICATION NUMBER:  PCT/US02/29001
; PRIOR FILING DATE:  2002-09-13
; PRIOR APPLICATION NUMBER:  US 10/243,552
; PRIOR FILING DATE:  2002-09-12
; PRIOR APPLICATION NUMBER:  US 60/322,511
; PRIOR FILING DATE:  2001-09-13
; PRIOR APPLICATION NUMBER:  PCT/US02/25485
; PRIOR FILING DATE:  2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS:  17116
; SOFTWARE:  pt FL_genes Version 6.0
; SEQ ID NO 10208
; LENGTH:  93
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-10-461-673-10208

Query Match      100.0%; Score 20; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 REDL 4
      ||||
Db      49 REDL 52

Search completed: March 20, 2006, 07:53:22
Job time : 17.5 secs
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; APPLICANT:  Xue, Aidong
; APPLICANT:  Wehrman, Tom
; APPLICANT:  Wang, Zhi Wei
; APPLICANT:  Yang, Yonghong
; APPLICANT:  Goodrich, Ryle W.
; APPLICANT:  Wang, Dunrui
; APPLICANT:  Yamazaki, Victoria
; APPLICANT:  Ujwal, Manusha L.
; APPLICANT:  Ma, Yunding
; APPLICANT:  Chen, Rui-Hong
; APPLICANT:  Ghosh, Malabika
; APPLICANT:  Weng, Gezhi
; APPLICANT:  Haley-Vicente, Dana
; APPLICANT:  Dmanac, Radoje T.
; TITLE OF INVENTION:  Novel Nucleic Acids and Polypeptides
; FILE REFERENCE:  823
; CURRENT APPLICATION NUMBER:  US/10/461,673
; CURRENT FILING DATE:  2003-06-13
; PRIOR APPLICATION NUMBER:  PCT/US02/29964
; PRIOR FILING DATE:  2002-09-19
; PRIOR APPLICATION NUMBER:  US 10/245,014
; PRIOR FILING DATE:  2002-09-16
; PRIOR APPLICATION NUMBER:  US 60/323,739
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; PRIOR APPLICATION NUMBER:  PCT/US02/29001
; PRIOR FILING DATE:  2002-09-13
; PRIOR APPLICATION NUMBER:  US 10/243,552
; PRIOR FILING DATE:  2002-09-12
; PRIOR APPLICATION NUMBER:  US 60/322,511
; PRIOR FILING DATE:  2001-09-13
; PRIOR APPLICATION NUMBER:  PCT/US02/25485
; PRIOR FILING DATE:  2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS:  17116
; SOFTWARE:  pt FL_genes Version 6.0
; SEQ ID NO 10208
; LENGTH:  93
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-10-461-673-10208

Query Match      100.0%; Score 20; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 REDL 4
      ||||
Db      78 REDL 81

RESULT 50
US-11-360-355-148045
; Sequence 148045, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT:  Boukharov, Andrey
; APPLICANT:  Du, Zijiang
; APPLICANT:  Guo, Liang
; APPLICANT:  Kovalic, David
; APPLICANT:  Lu, Maolong
; APPLICANT:  McCarter, James
; APPLICANT:  Miller, Nancy
; APPLICANT:  Williams, Deryck
; APPLICANT:  Vaudin, Mark
; APPLICANT:  Wu, Wei
; TITLE OF INVENTION:  METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE:  38-21(53885)
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:59 ; Search time 15 Seconds
(without alignments)
25.658 Million cell updates/sec

Title: US-09-673-707-10

Perfect score: 20

Sequence: 1 REDL 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	37	4	probable 2.8K prot
2	20	100.0	25	2	lignin peroxidase
3	20	100.0	50	2	tubulin alpha chain
4	20	100.0	51	2	ribosomal protein
5	20	100.0	53	2	tubulin alpha chain
6	20	100.0	59	2	nblA protein - Syn
7	20	100.0	67	2	14-3-3 protein iso
8	20	100.0	73	2	hypothetical prote
9	20	100.0	78	1	cytochrome c551 -
10	20	100.0	79	2	D-alanyl carrier p
11	20	100.0	81	2	probable plasmid s
12	20	100.0	83	2	hypothetical prote
13	20	100.0	84	2	hypothetical prote
14	20	100.0	85	2	probable involme
15	20	100.0	85	2	hypothetical prote
16	20	100.0	88	2	hypothetical prote
17	20	100.0	91	2	probable secreted
18	20	100.0	91	2	conserved hypothet
19	20	100.0	95	2	acyl carrier prote
20	20	100.0	97	2	translation initia
21	20	100.0	98	2	tubulin alpha chain
22	20	100.0	98	2	hypothetical prote
23	20	100.0	100	2	hypothetical prote
24	20	100.0	102	2	probable periplasm
25	20	100.0	103	2	phage-related, Zn
26	20	100.0	104	1	CCBO
27	20	100.0	104	1	cytochrome c - bov
28	20	100.0	104	1	cytochrome c [vali
29	20	100.0	104	1	cytochrome c - don
					cytochrome c - com

cytochrome c [vali
cytochrome c - she
cytochrome c, test
cytochrome c, test
hypothetical prote
hypothetical prote
glutaredoxin-like
pectin degradation
hypothetical prote
unknown protein en
hypothetical prote
glutaredoxin-like
transcription regu
transcription regu
Whcy protein - Ara
gas-vesicle operon
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
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serum amyloid A pr
translation repres
hypothetical prote
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conserved hypothet
hypothetical prote
thioredoxin N-2 -
hypothetical prote
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partial transposas
hypothetical prote
polyketide synthas
hypothetical prote
ribosomal protein
30S ribosomal prot
hypothetical prote
hypothetical prote
hypothetical prote
probable flagellar
transcription regu
hypothetical prote
probable esterase
hypothetical prote
very hypothetical
probable transcrip
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tropoin I alpha -
hypothetical prote
hypothetical prote
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
k11B protein - Str
ribosomal protein
conserved hypothet
conserved hypothet
ribosomal protein
ribosomal protein
ribosomal protein
ribosomal protein
hypothetical prote
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probable lyase - S
translation initia

103 20 100.0 153 2 AF1334
104 20 100.0 153 2 AE1705
105 20 100.0 153 2 I39827
106 20 100.0 153 2 S52083
107 20 100.0 153 2 E71526
108 20 100.0 153 2 C90405
109 20 100.0 154 1 A31486
110 20 100.0 154 1 FIHUA
111 20 100.0 154 2 T27228
112 20 100.0 154 2 F90394
113 20 100.0 155 1 D65197
114 20 100.0 155 2 T46546
115 20 100.0 155 2 T00134
116 20 100.0 156 1 W6WL41
117 20 100.0 156 2 F70027
118 20 100.0 157 2 S25479
119 20 100.0 158 2 A90085
120 20 100.0 161 1 UBURAL
121 20 100.0 161 2 C82272
122 20 100.0 161 2 E72339
123 20 100.0 162 1 Z3B8L7
124 20 100.0 162 2 Z3B8L7
125 20 100.0 162 1 C69424
126 20 100.0 162 2 G90288
127 20 100.0 163 2 A43259
128 20 100.0 164 2 S32867
129 20 100.0 164 2 C35216
130 20 100.0 164 2 F75616
131 20 100.0 164 2 S74709
132 20 100.0 166 1 B64019
133 20 100.0 166 2 D86026
134 20 100.0 167 2 E90329
135 20 100.0 168 2 T36405
136 20 100.0 169 2 D79928
137 20 100.0 171 2 D83443
138 20 100.0 171 2 T46342
139 20 100.0 172 2 D82194
140 20 100.0 172 2 A28713
141 20 100.0 172 2 AB1806
142 20 100.0 172 2 AB1434
143 20 100.0 172 2 A35145
144 20 100.0 172 2 D90346
145 20 100.0 173 2 T24720
146 20 100.0 173 2 A72714
147 20 100.0 173 2 AG3559
148 20 100.0 173 2 A82413
149 20 100.0 173 2 JC5610
150 20 100.0 174 2 AI1274

ALIGNMENTS

RESULT 1
JE0015
probable 2.8K protein pseudogene - cucumber mosaic virus (strain D)
C:Species: cucumber mosaic virus, CMV
C:Date: 31-Dec-1991 #sequence_revision 28-May-1998 #text_change 09-Jul-2004
C:Accession: JE0015; PS0286
R:Richards, K.E.; Jonard, G.; Jacquemond, M.; Lot, H.
Virology 89, 395-408, 1978
A:Title: Nucleotide sequence of cucumber mosaic virus-associated RNA 5.
A:Reference number: JE0015
A:Accession: JE0015
A:Status: translation not shown; conceptual translation of pseudogene
A:Molecule type: genomic RNA
A:Residues: 1-27 <RIC>
A:Cross-references: UNIPROT:Q89492; UNIPARC:UPI00000F7E7F
R:Kaper, J.M.; Touseignant, M.E.; Steen, M.T.
Virology 163, 284-292, 1988
A:Title: Cucumber mosaic virus-associated RNA 5. XI. Comparison of 14 CARNA 5 variants
A:Reference number: JE0018; MUID:88179532; PMID:3354198
A:Accession: PS0286

A:Status: translation not shown; conceptual translation of pseudogene
A:Molecule type: genomic RNA
A:Residues: 1-27 <KAP>
A:Cross-references: UNIPARC:UPI00000F7E7F; GB:M20350; NID:g331658; PIDN:AAA46385.1; PID
A:Note: this sequence is found in strain D and isolates Sq10, Ch20, X2nt3, X7, X12 and
C:Genetics:
A:Map position: segment 5
C:Keywords: pseudogene

Query Match 100.0%; Score 20; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 11 REDL 14

RESULT 2
S29728
lignin peroxidase (BC 1.11.1.-) 12 - white-rot fungus (Trametes versicolor) (fragment)
C:Species: Trametes versicolor (white-rot fungus)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 12-Jul-2004
C:Accession: S29728
R:Johansson, T.; Welinder, K.G.; Nyman, P.O.
Arch. Biochem. Biophys. 300, 57-62, 1993
A:Title: Isozymes of lignin peroxidase and manganese(II) peroxidase from the white-rot
ions.
A:Reference number: S29724; MUID:93143365; PMID:8424691
A:Accession: S29728
A:Molecule type: protein
A:Residues: 1-35 <JOH>
A:Cross-references: UNIPROT:Q9UQY7; UNIPARC:UPI0000069C2A
A:Experimental source: strain PRL 572
C:Function:
C:Superfamily: peroxidase
C:Keywords: extracellular protein; heme; oxidoreductase

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 22 REDL 25

RESULT 3
S36687
tubulin alpha chain - Blepharisma japonicum (fragment)
C:Species: Blepharisma japonicum
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: S36687
R:Liang, A.; Heckmann, K.
Naturwissenschaften 80, 225-226, 1993
A:Title: Blepharisma uses UAA as a termination codon.
A:Reference number: S36687; MUID:93288144; PMID:7685500
A:Accession: S36687
A:Molecule type: mRNA
A:Residues: 1-50 <LIA>
A:Cross-references: UNIPROT:Q08628; UNIPARC:UPI000013699B; GB:S623518; NID:g385736; PID
C:Genetics:
A:Genetic code: SGC9
C:Superfamily: tubulin
C:Keywords: heterodimer; microtubule

Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 11 REDL 14

Db 19 REDL 22

RESULT 4

C61510
ribosomal protein S18, cytosolic - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: C61510
R:Grosberger, D.; Flajnik, M.; Marcuz, A.
Comp. Biochem. Physiol. B 98, 127-133, 1991
A:Title: Ribosomal and chromosomal protein cDNA clones of Xenopus laevis thymus isolated
A:Reference number: A61510; MUID:91284580; PMID:2060276
A:Accession: C61510
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-51 <GR>
A:Cross-references: UNIPROT:Q7LZL4; UNIPARC:UPI00001772A1
C:Superfamily: ribosomal protein S13/S18

Query Match 100.0%; Score 20; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
7 REDL 10

RESULT 5

S71388
tubulin alpha chain - Giardia lamblia (fragments)
C:Species: Giardia lamblia
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 31-Dec-2004
C:Accession: S71388
R:Weber, K.; Schneider, A.; Mueller, N.; Plessmann, U.
FEBS Lett. 393, 27-30, 1996
A:Title: Polyglycylation of tubulin in the diplomonad Giardia lamblia, one of the oldest
A:Reference number: S71388; MUID:96397523; PMID:8804417
A:Accession: S71388
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-29;30-53 <WEB>
A:Cross-references: UNIPROT:Q9U014; UNIPARC:UPI0000177562; UNIPARC:UPI0000177563
C:Keywords: heterodimer; microtubule

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
21 REDL 24

RESULT 6

S42636
nblA protein - Synechococcus sp. (strain PCC 7942)
C:Species: Synechococcus sp.
A:Variety: PCC 7942
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S42636
R:Collier, J.L.; Grossman, A.R.
EMBO J. 13, 1039-1047, 1994
A:Title: A small polypeptide triggers complete degradation of light-harvesting phycobilin
A:Reference number: S42636; MUID:94178246; PMID:8131738
A:Accession: S42636
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-59 <COL>
A:Cross-references: UNIPROT:P35087; UNIPARC:UPI000012FDBC; GB:U05044; GB:U00671; NID:945
A:Experimental source: PCC 7942

Query Match 100.0%; Score 20; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
30 REDL 33

RESULT 7

S53754
14-3-3 protein isoform epsilon - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S53754
R:Jones, D.H.A.; Martin, H.; Madrazo, J.; Robinson, K.A.; Nielsen, P.; Roseboom, P.H.;
J. Mol. Biol. 245, 375-384, 1995
A:Title: Expression and structural analysis of 14-3-3 proteins.
A:Reference number: S53753; MUID:95139067; PMID:7837270
A:Accession: S53754
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-67 <JON>
A:Cross-references: UNIPROT:Q7M312; UNIPARC:UPI00001758B5
C:Superfamily: 14-3-3 protein

Query Match 100.0%; Score 20; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
4 REDL 7

RESULT 8

D90287
hypothetical protein SSO7675 [imported] - Sulfolobus solfataricus transposon ISC1316
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: D90287
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90287
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-73 <KUR>
A:Cross-references: UNIPROT:Q97YK4; UNIPARC:UPI0000064402; GB:AE006641; NID:gl3814523;
C:Genetics:
A:Gene: SSO7675

Query Match 100.0%; Score 20; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
10 REDL 13

RESULT 9

CCER51
cytochrome c551 - Ectothiorhodospira halophila
C:Species: Ectothiorhodospira halophila
C>Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C:Accession: S38755; A00115
R:Amblar, R.P.; Meyer, T.E.; Kamen, M.D.
Arch. Biochem. Biophys. 306, 83-93, 1993
A:Title: Amino acid sequences of cytochromes c-551 from the halophilic purple phototrop

Qy 1 REDL 4
||||
Db 46 REDL 49

RESULT 14

T39536
probable involvement in cytochrome oxidase assembly - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39536
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, February 1998
A:Reference number: 221862
A:Accession: T39536
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-85 <WOO>
A:Cross-references: UNIPROT:O42921; UNIPARC:UPI000006B7BF; EMBL:AL021748; PIDN:CAA16867.
A:Experimental source: strain 972h-; cosmid c16A3
C:Genetics:
A:Gene: SPDB:SPBC16A3.16
A:Map position: 2
A:Introns: 57/3

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
||||
Db 9 REDL 12

RESULT 15

T26542
hypothetical protein Y19D2B.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26542
R:White, S.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z20227
A:Accession: T26542
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-85 <WIL>
A:Cross-references: UNIPROT:Q9XXH2; UNIPARC:UPI000007EA87; EMBL:AL023832; PIDN:CAA19475.
A:Experimental source: clone Y19D2B
C:Genetics:
A:Gene: CESP:Y19D2B.1
A:Map position: 2
A:Introns: 42/2

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
||||
Db 57 REDL 60

RESULT 16

F83979
hypothetical protein BH2638 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: F83979
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83979
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <STO>
A:Cross-references: UNIPROT:Q9K9K7; UNIPARC:UPI000013BEA1; GB:AP001516; GB:BA000004; N
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2638

Query Match 100.0%; Score 20; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
||||
Db 36 REDL 39

RESULT 17

AE0547
probable secreted protein [imported] - Salmonella enterica subsp. enterica serovar Typhi
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AE0547
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0547
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <PAR>
A:Cross-references: UNIPARC:UPI000005A269; GB:AL513382; PIDN:CAD08821.1; PID:gi6501635
C:Genetics:
A:Gene: STY0398
C:Superfamily: conserved hypothetical protein b3238

Query Match 100.0%; Score 20; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
||||
Db 55 REDL 58

RESULT 18

E83483
conserved hypothetical protein PA1298 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: E83483
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; L
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liu
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83483
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:Q9I446; UNIPARC:UPI00000C52F9; GB:AE004559; GB:AE004091; NI
A:Experimental source: strain PA01
C:Genetics:
C:Superfamily: hypothetical protein b2105

Query Match 100.0%; Score 20; DB 2; Length 91;

```
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
    ||||
DB 76 REDL 79

RESULT 19
A47030
A;Title: carrier protein - Saccharopolyspora erythraea
C;Species: Saccharopolyspora erythraea
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A47030; S00186
R;Revill, W.P.; Leadlay, P.F.
J. Bacteriol. 173, 4379-4385, 1991
A;Title: Cloning, characterization, and high-level expression in Escherichia coli of the
sis.
A;Reference number: A47030; MUID:91294181; PMID:2066335
A;Accession: A47030
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <REV>
A;Cross-references: UNIPROT:P11830; UNIPARC:UPI0000125383; GB:M64477; NID:g152677; PIDN:
R;Hale, R.S.; Jordan, K.N.; Leadlay, P.F.
FEBS Lett. 224, 133-136, 1987
A;Title: A small, discrete acyl carrier protein is involved in de novo fatty acid biosyn
A;Reference number: S00186; MUID:88055578; PMID:3315744
A;Accession: S00186
A;Molecule type: protein
A;Residues: 1-31,'X','33-44','X',46 <HAL>
A;Cross-references: UNIPARC:UPI0000177FC6
A;Note: the source is designated as Streptomyces erythraeus
C;Comment: This protein is the carrier of the growing fatty acid chain in fatty acid syn
C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C;Keywords: carrier protein; fatty acid biosynthesis; lipid metabolism; phosphopantethei
F;4-75/Domain: acyl carrier protein homology <ACP>
F;39/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 100.0%; Score 20; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
    ||||
DB 32 REDL 35

RESULT 20
B42156
translation initiation factor eIF-5A II [validated] - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 18-Aug-2000
C;Accession: B42156
R;Wolff, E.C.; Kinzy, T.G.; Merrick, W.C.; Park, M.H.
J. Biol. Chem. 267, 6107-6113, 1992
A;Title: Two isoforms of eIF-5A in chick embryo. Isolation, activity, and comparison of
A;Reference number: A42156; MUID:92210582; PMID:1556119
A;Accession: B42156
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-97 <WOL>
A;Cross-references: UNIPARC:UPI00001782DA
C;Superfamily: translation initiation factor eIF-5A
C;Keywords: hypusine; protein biosynthesis
F;26/Modified site: N6-(4-amino-2-hydroxybutyl)lysine (Lys) #status experimental

Query Match 100.0%; Score 20; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
    ||||
```

```
DB 85 REDL 88

RESULT 21
I57601
tubulin alpha chain isotype H2-alpha - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I57601
R;Villasante, A.; Wang, D.; Dobner, P.; Dolph, P.; Lewis, S.A.; Cowan, N.J.
Mol. Cell. Biol. 6, 2409-2419, 1986
A;Title: Six mouse alpha-tubulin mRNAs encode five distinct isotypes: Testis-specific e
A;Reference number: I57601; MUID:87064538; PMID:3785200
A;Accession: I57601
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-98 <RES>
A;Cross-references: UNIPROT:Q15670; UNIPARC:UPI00000706A3; GB:K03460; NID:g340016; PIDN:
C;Superfamily: tubulin

Query Match 100.0%; Score 20; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
    ||||
DB 70 REDL 73

RESULT 22
B95323
hypothetical protein SMA0894 [imported] - Sinorhizobium meliloti (strain 1021) magaplas
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95323
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9886, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: B95323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <KUR>
A;Cross-references: UNIPROT:Q92ZJ5; UNIPARC:UPI000000C80E3; GB:AE006469; PIDN:AAK65148.1
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMA0894
A;Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
    ||||
DB 22 REDL 25

RESULT 23
S69860
hypothetical protein YML116w-a - Yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
```


C;Accession: S69860
R;Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S53954
A;Accession: S69860
A;Molecule type: DNA
A;Residues: 1-100 <SK>
A;Cross-references: UNIPARC:UPI00001683B6; EMBL:Z49210; GSPDB:GN00013; MIPS:YML116w-a
C;Genetics:
A;Gene: MIPS:YML116w-a
A;Map position: 13L
C;Superfamily: Saccharomyces hypothetical protein YML116w-a

Query Match 100.0%; Score 20; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 11 REDL 14

RESULT 24
C71091
probable periplasmic divalent cation tolerance protein CutA - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: C71091
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71091
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-102 <KAW>
A;Cross-references: UNIPROT:Q58720; UNIPARC:UPI000006682A; GB:AP000004; NID:G3236131; PI
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0992

Query Match 100.0%; Score 20; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 58 REDL 61

RESULT 25
A97134
phage-related, Zn finger domain containing protein [imported] - Clostridium acetobutylic
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004
C;Accession: A97134
R;Nolling, J.; Breston, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97134
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <KUR>
A;Cross-references: UNIPROT:Q97HW0; UNIPARC:UPI00000CA348; GB:AE001437; PIDN:AAK79860.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1897
C;Superfamily: HNH endonuclease, phi-105 (gp19) type

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 54 REDL 57

RESULT 26
CC80
cytochrome c - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C;Accession: A92022; A00007
R;Nakashima, T.; Higa, H.; Matsubara, H.; Benson, A.; Yasunobu, K.T.
J. Biol. Chem. 241, 1166-1177, 1966
A;Title: The amino acid sequence of bovine heart cytochrome c.
A;Reference number: A92022; MUID:66132521; PMID:5933874
A;Accession: A92022
A;Molecule type: protein
A;Residues: 1-104 <NAK>
A;Cross-references: UNIPROT:P00006; UNIPARC:UPI0000128B9A
R;Tsunabawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A;Title: Micro-identification of amino-terminal acetylamino acids in proteins.
A;Reference number: A61297; MUID:83056735; PMID:6754709
A;Contents: annotation; acetylation
C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallo
F;4-98/Domain: cytochrome c homology <CYC>
F;1/Modified site: acetylated amino end (Gly) #status experimental
F;14,17/Binding site: heme (Cys) (covalent) #status predicted
F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 91 REDL 94

RESULT 27
CCHO
cytochrome c [validated] - horse
C;Species: Equus caballus (domestic horse)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Dec-2004
C;Accession: A00005; S59487
R;Margoliash, E.; Smith, E.L.; Kreil, G.; Tuppy, H.
Nature 192, 1125-1127, 1961
A;Title: The complete amino-acid sequence.
A;Reference number: A93145
A;Accession: A00005
A;Molecule type: protein
A;Residues: 1-104 <MAR>
A;Cross-references: UNIPROT:P00004; UNIPARC:UPI000011054E
R;Theodorakis, J.B.; Arnes, L.G.; Margoliash, E.
Biochim. Biophys. Acta 1252, 114-125, 1995
A;Title: beta-Thiopropionyl cytochromes c modified at lysyl residues: preparation and c
A;Reference number: S59487; MUID:96001358; PMID:7548153
A;Accession: S59487
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10;11-18;19-26;27-34;38-47;50-54;55-58;60-67;68-74;75-82;83-97;98-104 <TH
A;Cross-references: UNIPARC:UPI0000171C7B; UNIPARC:UPI0000171C7C; UNIPARC:UPI0000171C7D;
C82; UNIPARC:UPI0000171C83; UNIPARC:UPI0000171C84; UNIPARC:UPI0000171C85; UNIPARC:UPI0000171C86;
R;Luo, Y.; Brayer, G.D.
submitted to the Brookhaven Protein Data Bank, August 1994
A;Reference number: A52805; PDB:1HRC
A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 1-104
R;Dickerson, R.E.; Takano, T.; Eisenberg, D.; Kallai, O.B.; Samson, L.; Cooper, A.; Mar

J. Biol. Chem. 246, 1511-1533, 1971
 A;Title: Ferricytochrome c. I. General features of the horse and bonito proteins at 2.8
 A;Reference number: A92076; MUID:71116428; PMID:5545094
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms
 C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
 C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloproteins
 F;4-98/Domain: cytochrome c homology <CYC>
 F;1/Modified site: acetylated amino end (Gly) #status experimental
 F;14,17/Binding site: heme (Cys) (covalent) #status experimental
 F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status experimental

Query Match 100.0%; Score 20; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 91 REDL 94

RESULT 28
 CCHOD
 cytochrome c - donkey (tentative sequence)
 C;Species: Equus asinus (donkey)
 C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 31-Dec-2004
 C;Accession: A00006
 R;Wlasek, O.F.; Margolias, E.
 J. Biol. Chem. 252, 830-834, 1977
 A;Title: Transimission of the cytochrome c structural gene in horse-donkey crosses.
 A;Reference number: A92217; MUID:77118552; PMID:190219
 A;Accession: A00006
 A;Molecule type: protein
 A;Residues: 1-104 <WAL>
 A;Cross-references: UNIPROT:P00005; UNIPARC:UPI0000128BB1
 A;Note: compositions of chymotryptic peptides and the sequence of residues 47-48 were determined
 A;Note: mules and hinnies are heterozygous, having equal amounts of horse and donkey cytochrome c
 C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
 C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloproteins
 F;4-98/Domain: cytochrome c homology <CYC>
 F;1/Modified site: acetylated amino end (Gly) #status predicted
 F;14,17/Binding site: heme (Cys) (covalent) #status predicted
 F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 91 REDL 94

RESULT 29
 CCHOD
 cytochrome c - common zebra (tentative sequence)
 C;Species: Equus burchelli, Equus quagga (common zebra, plains zebra)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
 C;Accession: A91330; A00006
 R;Guertler, L.; Horstmann, H.J.
 FEBS Lett. 18, 106-108, 1971
 A;Title: Zur Primärstruktur des Cytochromes c des Steppenzebras (Equus quagga boehmi).
 A;Reference number: A91330
 A;Accession: A91330
 A;Molecule type: protein
 A;Residues: 1-104 <GUES>
 A;Cross-references: UNIPROT:P00005; UNIPARC:UPI0000128BB1
 A;Note: the amino acid composition and the sequence of residues 40-48 were determined
 C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
 C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloproteins
 F;4-98/Domain: cytochrome c homology <CYC>
 F;1/Modified site: acetylated amino end (Gly) #status predicted
 F;14,17/Binding site: heme (Cys) (covalent) #status predicted
 F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 91 REDL 94

RESULT 30
 CCHOD
 cytochrome c [validated] - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 31-Dec-2004
 C;Accession: A00007
 R;Stewart, J.W.; Margolias, E.
 Can. J. Biochem. 43, 1187-1206, 1965
 A;Title: The primary structure of the cytochrome c from various organs of the hog.
 A;Reference number: A90743; MUID:66072936; PMID:5855656
 A;Accession: A00007
 A;Molecule type: protein
 A;Residues: 1-104 <STE>
 A;Cross-references: UNIPROT:P00006; UNIPARC:UPI0000128B9A
 C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
 C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloproteins
 F;4-98/Domain: cytochrome c homology <CYC>
 F;1/Modified site: acetylated amino end (Gly) #status experimental
 F;14,17/Binding site: heme (Cys) (covalent) #status experimental
 F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 91 REDL 94

RESULT 31
 CCHOD
 cytochrome c - sheep (tentative sequence)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
 C;Accession: A91454; A00007
 R;Smith, E.L.; Margolias, E.
 Fed. Proc. 23, 1243-1247, 1964
 A;Title: Evolution of cytochrome c.
 A;Reference number: A91454
 A;Accession: A91454
 A;Molecule type: protein
 A;Residues: 1-104 <SMI>
 A;Cross-references: UNIPROT:P00006; UNIPARC:UPI0000128B9A
 A;Note: amino acid compositions and mobilities of tryptic and chymotryptic peptides were determined
 C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
 C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloproteins
 F;4-98/Domain: cytochrome c homology <CYC>
 F;1/Modified site: acetylated amino end (Gly) #status predicted
 F;14,17/Binding site: heme (Cys) (covalent) #status predicted
 F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
 ||||
 Db 91 REDL 94

RESULT 32
 CCHOD
 cytochrome c - sheep (tentative sequence)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
 C;Accession: A91454; A00007
 R;Smith, E.L.; Margolias, E.
 Fed. Proc. 23, 1243-1247, 1964
 A;Title: Evolution of cytochrome c.
 A;Reference number: A91454
 A;Accession: A91454
 A;Molecule type: protein
 A;Residues: 1-104 <SMI>
 A;Cross-references: UNIPROT:P00006; UNIPARC:UPI0000128B9A
 A;Note: amino acid compositions and mobilities of tryptic and chymotryptic peptides were determined
 C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
 C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloproteins
 F;4-98/Domain: cytochrome c homology <CYC>
 F;1/Modified site: acetylated amino end (Gly) #status predicted
 F;14,17/Binding site: heme (Cys) (covalent) #status predicted
 F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

cytochrome c, testis-specific [validated] - mouse
N:Alternate names: cytochrome c
C:Species: Mus musculus (house mouse)
C>Date: 24-Apr-1984 #sequence revision 30-Sep-1991 #text_change 31-Dec-2004
C:Accession: B28160; A00012; I48313
R:Virbasius, J.V.; Scarpulla, R.C.
J. Biol. Chem. 263, 6791-6796, 1988
A:Title: Structure and expression of rodent genes encoding the testis-specific cytochrome c
A:Reference number: A28160; MUID:88198250; PMID:2834389
A:Accession: B28160
A:Molecule type: mRNA
A:Residues: 1-105 <VR>
A:Cross-references: UNIPROT:P00015; UNIPARC:UPI0000022AAF; GB:M20625; NID:g192875; PIDN:E71634
R:Hennig, B.
Eur. J. Biochem. 55, 167-183, 1975
A:Title: Change of cytochrome c structure during development of the mouse.
A:Reference number: A00012; MUID:76022386; PMID:240690
A:Accession: A00012
A:Molecule type: protein
A:Residues: 2-57, 'IV', 60-61, 'ZZ', 64-66, 'Z', 68-69, 'ZB', 72-105 <HEN>
A:Cross-references: UNIPARC:UPI0000171C87
A:Experimental source: strain BALB/c
R:Hake, L.E.; Alcivar, A.A.; Hecht, N.B.
Development 110, 249-257, 1990
A:Title: Changes in mRNA length accompany translational regulation of the somatic and testis-specific cytochrome c
A:Reference number: I48313; MUID:91184013; PMID:1964409
A:Accession: I48313
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-105 <RES>
A:Cross-references: UNIPARC:UPI0000022AAF; EMBL:X55771; NID:g288155; PIDN:CAA39293.1; PIDN:CAA39293.1; PIDN:CAA39293.1
C:Comment: Mammalian testis contains two forms of cytochrome c, one identical with the embryonic form and the other identical with the adult form.
C:Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
C:Keywords: blocked amino end; chromoprotein; electron transfer; heme; iron; metalloprotein
F:2-105/Product: cytochrome c, testis-specific #status experimental <MAT>
F:5-99/Domain: cytochrome c homology <CYC>
F:2/Modified site: blocked amino end (Gly) (in mature form) (probably acetylated) #status experimental
F:15,18/Binding site: heme (Cys) (covalent) #status experimental
F:19,81/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 92 REDL 95

RESULT 33
CCRTT
Cytochrome c, testis-specific - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 31-Dec-2004
C:Accession: A28160
R:Virbasius, J.V.; Scarpulla, R.C.
J. Biol. Chem. 263, 6791-6796, 1988
A:Title: Structure and expression of rodent genes encoding the testis-specific cytochrome c
A:Reference number: A28160; MUID:88198250; PMID:2834389
A:Accession: A28160
A:Molecule type: DNA; mRNA
A:Residues: 1-105 <VR>
A:Cross-references: UNIPROT:P10715; UNIPARC:UPI0000167AA4; GB:M20627; GB:M20628; NID:g20627; GB:M20627; GB:M20628
C:Comment: Mammalian testis contains two forms of cytochrome c, one identical to the embryonic form and the other identical to the adult form.
C:Genetics: 57/1
A:Introns: 57/1
C:Superfamily: cytochrome c/cytochrome c2; cytochrome c homology
C:Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloprotein
F:2-105/Product: cytochrome c, testis-specific #status predicted <MAT>
F:5-99/Domain: cytochrome c homology <CYC>
F:2/Modified site: acetylated amino end (Gly) (in mature form) #status predicted

F:15,18/Binding site: heme (Cys) (covalent) #status predicted
F:19,81/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 92 REDL 95

RESULT 34
A72465
hypotheical protein APE2364 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72465
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72465
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <KAW>
A:Cross-references: UNIPROT:Q9Y9C3; UNIPARC:UPI000005E2FD; DDBJ:AP000064; NID:g5105945
A:Experimental source: strain K1
C:Genetics:
C:Superfamily: Aeropyrum pernix hypotheical protein APE2364

Query Match 100.0%; Score 20; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 31 REDL 34

RESULT 35
AD0106
hypotheical protein YPO0865 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD0106
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <KUR>
A:Cross-references: UNIPROT:Q8ZHM6; UNIPARC:UPI00000DC736; GB:AL590842; PIDN:CAC89711.
C:Genetics:
A:Gene: YPO0865

Query Match 100.0%; Score 20; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 46 REDL 49

RESULT 36
E71634

glutaredoxin-like protein grLA (grxC2) RP745 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 05-Oct-2004
C:Accession: E71634
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichertz-Ponten, T.; Alemark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: E71634
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-107 <AND>
A:Cross-references: UNIPROT:O05957; UNIPARC:UPI000012BAE8; GB:AJ235269; NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: grxC2; RP745
C:Superfamily: monothiol glutaredoxin

Query Match 100.0%; Score 20; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||||
DB 61 REDL 64

RESULT 37
G71149
hypothetical protein PH0409 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: G71149
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: G71149
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-107 <KAW>
A:Cross-references: UNIPROT:O58146; UNIPARC:UPI0000062DE4; GB:AP0000002; NID:G3236129; PI
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0409

Query Match 100.0%; Score 20; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||||
DB 24 REDL 27

RESULT 38
H83711
pectin degradation protein kgf [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: H83711
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H83711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <STO>
A:Cross-references: UNIPROT:Q9KFI3; UNIPARC:UPI00000C38D0; GB:AP001508; GB:BA000004; NID
A:Experimental source: strain C-125

C:Genetics:
A:Gene: kgf
C:Superfamily: involved in pectin degradation

Query Match 100.0%; Score 20; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||||
DB 98 REDL 101

RESULT 39
H90875
hypothetical protein ECs1976 [imported] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H90875
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gabayara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAY>
A:Cross-references: UNIPROT:O8X2M1; UNIPARC:UPI00000D2AAL; GB:BA0000007; PIDN:BAB35399.1
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: ECs1976
C:Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 20; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||||
DB 83 REDL 86

RESULT 40
F85691
unknown protein encoded by prophage CP-933X [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85691
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85691
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <STO>
A:Cross-references: UNIPROT:O8X4P1; UNIPARC:UPI00000D0DA4; GB:AE005174; NID:g12514831;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1901
C:Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 20; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||||
DB 83 REDL 86

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RESULT 41
A99822
hypothetical protein ECs1545 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A99822
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A99822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAY>
A:Cross-references: UNIPROT:Q8X4P1; UNIPARC:UPI00000D0DA4; GB:BA000007; PIDN:BA034968.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs1545
C:Superfamily: uncharacterized conserved protein

Query Match      100.0%; Score 20; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      83 REDL 86

RESULT 42
D97843
glutaredoxin-like protein grla [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004
C:Accession: D97843
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: D97843
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <KUR>
A:Cross-references: UNIPROT:Q92GH5; UNIPARC:UPI00000C0BF5; GB:AE006914; PIDN:AAL03686.1;
C:Genetics:
A:Gene: grxC2
C:Superfamily: monothiol glutaredoxin

Query Match      100.0%; Score 20; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      65 REDL 68

RESULT 43
T35131
transcription regulator - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35131
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21568
A:Accession: T35131
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-111 <SEE>
A:Cross-references: UNIPROT:Q8CJQ4; UNIPARC:UPI000017AE11; EMBL:AL022268; PIDN:CAA18347.
A:Experimental source: strain A3(2)

```

C:Genetics:

A:Gene: SC0EDB:SC4H2.32

Query Match 100.0%; Score 20; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

||||

Db 90 REDL 93

RESULT 44

AE2039

transcription regulator alr1867 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AE2039

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasaemoto, S.; Watanabe, A.; Iriugu-

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2039

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: UNIPROT:Q8YVW6; UNIPARC:UPI00000CE231; GB:BA000019; PIDN:BA073566.

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr1867

C:Superfamily: arsenical resistance operon repressor

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 112;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

||||

Db 81 REDL 84

RESULT 45

S00006

Whey protein - Arabian camel

C:Species: Camelus dromedarius (Arabian camel)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C:Accession: S00006

R:Beq, O.U.; von Bahr-Lindstroem, H.; Zaidi, Z.H.; Joernvall, H.

FEBS Lett. 216, 270-274, 1987

A:Title: Characterization of a heterogeneous camel milk whey non-casein protein.

A:Reference number: S00006; MUID:87219156; PMID:3495459

A:Accession: S00006

A:Molecule type: protein

A:Residues: 1-112 <BSG>

A:Cross-references: UNIPROT:P15522; UNIPARC:UPI00001797D0

A:Note: the sequence Ala-Ala-Gln-Val-Glu-Ile was also found for residues 4-9

C:Comment: N-terminal fragments derived from both mature protein variants were also fo

C:Keywords: milk

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 112;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

||||

Db 17 REDL 20

RESULT 46

JQ1128

gas-vesicle operon protein gvpK - Halobacterium salinarum plasmids pHH1 and pNRC100

C;Species: Halobacterium salinarum
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Jan-2000
C;Accession: JQ1128; S15190
R;Jones, J.G.; Young, D.C.; DasSarma, S.
Gene 102, 117-122, 1991
A;Title: Structure and organization of the gas vesicle gene cluster on the Halobacterium
A;Reference number: JQ1122; MUID:91323716; PMID:1864501
A;Accession: JQ1128
A;Molecule type: DNA
A;Residues: 1-113 <ON>
A;Cross-references: UNIPARC:UPI000012BE37; GB:M58557; NID:g150406; PID:g455299
A;Experimental source: strain NRC-1, plasmid pNRC100
A;Genetics: NRC
A;Note: the source is designated as Halobacterium halobium
R;Horne, M.; Engleert, C.; Wimmer, C.; Pfeifer, F.
Mol. Microbiol. 5, 1159-1174, 1991
A;Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in
A;Reference number: S15183; MUID:92065812; PMID:1956294
A;Accession: S15190
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-113 <HOR>
A;Cross-references: UNIPARC:UPI000012BE37; EMBL:X55648; NID:g43516; PID:g43524
A;Experimental source: plasmid pHH1
A;Genetics: PHH
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1990
C;Genetics: <NRC>
A;Gene: gvpK
A;Genome: plasmid pNRC100
C;Genetics: <PHH>
A;Gene: gvpK
A;Genome: plasmid pHH1

Query Match 100.0%; Score 20; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 80 REDL 83

RESULT 47
T08234
gas-vesicle operon protein gvpK - Halobacterium sp. (strain NRC-1) plasmid pNRC100
N;Alternate names: hypothetical protein H0228
C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R;Ng, W.V.; Ciufu, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m
A;Reference number: Z16408; MUID:99063795; PMID:9847077
A;Accession: T08234
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-113 <NGW>
A;Cross-references: UNIPROT:P24375; UNIPARC:UPI000012BE37; EMBL:AF016485; NID:g2822278;
A;Experimental source: strain NRC-1
C;Genetics:
A;Gene: gvpK; HALOSP:H0228
A;Genome: plasmid pNRC100

Query Match 100.0%; Score 20; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 80 REDL 83

RESULT 48
G83746
hypothetical protein BH0775 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83746
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83746
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <STO>
A;Cross-references: UNIPROT:Q9KES4; UNIPARC:UPI00000C39AB; GB:BA001509; GB:BA000004; NI
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0775

Query Match 100.0%; Score 20; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 72 REDL 75

RESULT 49
G95059
hypothetical protein SP0514 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95059
R;Tettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
on, J.D.; Hickay, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, S.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95059
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <KUR>
A;Cross-references: UNIPROT:Q97S74; UNIPARC:UPI0000051481; GB:AE005672; PIDN:AAK74672.1
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0514

Query Match 100.0%; Score 20; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 79 REDL 82

RESULT 50
E83395
hypothetical protein PA1995 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Li
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liu
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pat
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83395

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-118 <STO>
 A;Cross-references: UNIPROT:Q9I2B4; UNIPARC:UPI000000C554A; GB:AE004626; GB:AE004091; NID
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA1995

Query Match 100.0%; Score 20; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 ||||
 Db 17 REDL 20

Search completed: March 20, 2006, 07:50:44
 Job time : 18 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:50 ; Search time 147.5 Seconds
(without alignments)
19.133 Million cell updates/sec

Title: US-09-673-707-10
Perfect score: 20
Sequence: 1 REDL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	27	Q89492	cucumber mo
2	20	100.0	29	Q86LH9	9METZ
3	20	100.0	30	Q4YF88	PLABE
4	20	100.0	31	Q4KA34	PSEES
5	20	100.0	32	Q86LH9	9METZ
6	20	100.0	34	Q95LA6	PIC
7	20	100.0	35	Q9UQV7	TRAVE
8	20	100.0	35	Q570E3	ARATH
9	20	100.0	35	Q5NQJ6	ZVMMO
10	20	100.0	36	Q9QW57	9MURI
11	20	100.0	38	Q56Y22	ARATH
12	20	100.0	39	Q19688	HUMAN
13	20	100.0	39	Q61645	APLCA
14	20	100.0	39	Q8MTM6	9DIPT
15	20	100.0	39	Q74264	9HIVI
16	20	100.0	41	Q9UW29	9PEZI
17	20	100.0	41	Q8CH67	MOUSE
18	20	100.0	45	Q8WMC5	PONPY
19	20	100.0	45	Q8WNI7	HYLKL
20	20	100.0	45	Q84U35	9ASPA
21	20	100.0	46	Q8UT46	9NOGA
22	20	100.0	46	Q8WNI7	CERAE
23	20	100.0	47	Q87Z84	9ESM
24	20	100.0	49	Q4GXQ0	9COLE
25	20	100.0	49	Q7YQ54	PHOSS
26	20	100.0	49	Q7YQ55	PHOSS
27	20	100.0	49	Q7YQ56	PHOSS
28	20	100.0	49	Q7YQ57	PHOSS
29	20	100.0	49	Q7YQ58	PHOSS
30	20	100.0	49	Q7YQ59	PHOSS
31	20	100.0	49	Q7YQ60	PHOSS

32	20	100.0	49	2	Q4ZR70	PSESY
33	20	100.0	50	1	TBA	BLEJA
34	20	100.0	50	2	Q4XG11	PLACH
35	20	100.0	50	2	Q7ZT89	CARAU
36	20	100.0	51	2	Q64BT2	9ARCH
37	20	100.0	51	2	Q8NFP0	HUMAN
38	20	100.0	51	2	Q7LZL4	XENLA
39	20	100.0	52	2	Q8MZQ7	9DIPT
40	20	100.0	52	2	Q58LK4	9CAUD
41	20	100.0	52	2	Q5XY22	BORGA
42	20	100.0	54	2	Q96XL7	SULTO
43	20	100.0	54	2	Q9GLJ2	PIC
44	20	100.0	54	2	Q94KJ8	PINTA
45	20	100.0	54	2	Q69433	9BACI
46	20	100.0	54	2	Q69233	BACCE
47	20	100.0	55	2	Q5QLQ2	ORYSA
48	20	100.0	55	2	Q8F9U9	LEPIN
49	20	100.0	56	2	Q5E042	VIBFI
50	20	100.0	57	2	Q4HAV9	9DEIO
51	20	100.0	58	2	Q7MJF3	VIBVY
52	20	100.0	59	1	NBLA	SYNP7
53	20	100.0	59	2	Q5TUH5	ANOGA
54	20	100.0	59	2	Q8SZB9	9DROM
55	20	100.0	60	2	Q4X922	PLACH
56	20	100.0	60	2	Q653Q0	ORYSA
57	20	100.0	62	2	Q8WME7	PONPY
58	20	100.0	62	2	Q8WNI7	HYLKL
59	20	100.0	63	2	Q8WNI7	CERAE
60	20	100.0	63	2	Q9XSB0	BOVIN
61	20	100.0	63	2	Q65EM4	BACLD
62	20	100.0	64	2	Q8VT56	STRMU
63	20	100.0	64	2	Q5N0L5	SYNP6
64	20	100.0	64	2	Q4RA80	TETNG
65	20	100.0	64	2	Q7L431	9HIVI
66	20	100.0	66	1	RL29	SILPO
67	20	100.0	66	2	Q77FS8	9CAUD
68	20	100.0	66	2	Q9MBY4	9CAUD
69	20	100.0	66	2	Q6YQ72	ONYPE
70	20	100.0	66	2	Q9QW45	9MURI
71	20	100.0	67	2	Q647X2	9ARCH
72	20	100.0	67	2	Q7M312	SHEEP
73	20	100.0	67	2	Q9XJU6	9CAUD
74	20	100.0	67	2	Q9F2D2	SALTY
75	20	100.0	67	2	Q9AN11	BRAJA
76	20	100.0	68	2	Q5P601	9AZOSE
77	20	100.0	68	2	Q9IF22	9HIVI
78	20	100.0	69	2	Q01723	BRABL
79	20	100.0	69	2	Q9JN70	BACCE
80	20	100.0	69	2	Q9IF24	9HIVI
81	20	100.0	69	2	Q71476	9HIVI
82	20	100.0	71	2	Q5Y1B6	9Z2Z2
83	20	100.0	71	2	Q66L18	XENLA
84	20	100.0	72	2	Q52UL4	BOVIN
85	20	100.0	72	2	Q4UK11	RICFE
86	20	100.0	72	2	Q9IF04	9HIVI
87	20	100.0	73	2	Q97YK4	SULSO
88	20	100.0	73	2	Q50014	MYCLE
89	20	100.0	73	2	Q4MMB8	BACCE
90	20	100.0	74	2	Q7S2A0	NEUCR
91	20	100.0	74	2	Q9IF06	9HIVI
92	20	100.0	74	2	Q5V382	HALMA
93	20	100.0	75	2	Q84K97	9ASPA
94	20	100.0	75	2	Q82QL9	STRAM
95	20	100.0	75	2	Q8VKG6	MYCTU
96	20	100.0	76	2	Q5YVR1	NOCPA
97	20	100.0	76	2	Q81X92	BACAN
98	20	100.0	76	2	Q4RC99	TETNG
99	20	100.0	76	2	Q5Z8F0	ORVSA
100	20	100.0	77	2	Q9RLF4	PLARU
101	20	100.0	77	2	Q4NPF2	9MICC
102	20	100.0	77	2	Q7M6V4	MOUSE
103	20	100.0	77	2	Q91F25	9GVCP
104	20	100.0	77	2		

Q4ZR70	pseudomonas
Q86628	blepharisma
Q4XG11	plasmidium
Q7ZT89	carassius a
Q64BT2	uncultured
Q8NFP0	homo sapien
Q7LZL4	xenopus lae
Q8MZQ7	drosophila
Q58LK4	cyanophage
Q5XY22	borrelia ga
Q96XL7	sulfolobus
Q9GLJ2	sus scrofa
Q94KJ8	pinus taeda
Q69433	exiguobacte
Q69233	exiguobacte
Q5QLQ2	oryza sativ
Q8F9U9	leptospira
Q5E042	vibrio fisc
Q4HAV9	deinococcus
Q7MJF3	vibrio vuln
P35087	synecococc
Q5TUH5	anopheles g
Q8SZB9	drosophila
Q4X922	plasmidium
Q653Q0	oryza sativ
Q8WME7	pongo pygma
Q8WNI7	hylobates k
Q8WNI7	hylobates k
Q9XSB0	bos taurus
Q65EM4	bacillus li
Q8VT56	streptococc
Q5N0L5	synecococc
Q4RA80	tetraodon n
Q7L431	human immun
Q5LW50	silicibacte
Q77PS8	streptococc
Q9MBY4	streptococc
Q6YQ72	onion yello
Q9QW45	rattus sp.
Q647X2	uncultured
Q7M312	ovis aries
Q9XJU6	streptococc
Q9F2D2	salmonella
Q9AN11	bradyrhizob
Q5P601	azococcus sp
Q9IF22	human immun
Q01723	branchiosto
Q9JN70	bacillus ce
Q9IF24	human immun
Q71476	human immun
Q5Y1B6	uncultured
Q66L18	xenopus lae
Q52UL4	bos taurus
Q4UK11	rickettsia
Q9IF04	human immun
Q97YK4	sulfolobus
Q50014	mycobacteri
Q4MMB8	bacillus ce
Q7S2A0	neurospora
Q61L77	drosophila
Q9IF06	human immun
Q5V382	haloarcua
Q84K97	crocus sati
Q82QL9	streptomyce
Q8VKG6	mycobacteri
Q5YVR1	nocardia fa
Q81X92	bacillus an
Q4RC99	tetraodon n
Q5Z8F0	oryza sativ
Q9RLF4	planktothri
Q4NPF2	arthrobact
Q7M6V4	mus musculu
Q91F25	cydia pomon

105	20	100.0	78	1	CY551_ECTHA	P00122 ectothiorho						
106	20	100.0	78	2	Q6PPD8_HELAM	Q6PPD8 helicoverpa						
107	20	100.0	78	2	Q75H75_ORYSA	Q75H75 oryza sativ						
108	20	100.0	78	2	Q8D105_SYNEL	Q8D105 synecococc						
109	20	100.0	79	1	DLTC_ABIDE	Q8G169 abiotrophia						
110	20	100.0	79	1	DLTC_LACLA	Q9C951 lactococcus						
111	20	100.0	79	2	Q64CH6_9ARCH	Q64CH6 uncultured						
112	20	100.0	79	2	Q4T7Q6_TETNG	Q4T7Q6 tetraodon n						
113	20	100.0	79	2	Q9IF14_9HIV1	Q9IF14 human immun						
114	20	100.0	80	2	Q8NKP1_SULAC	Q8NKP1 sulfolobus						
115	20	100.0	80	2	Q53QY5_HUMAN	Q53QY5 homo sapien						
116	20	100.0	80	2	Q87T24_VIBPA	Q87T24 vibrio para						
117	20	100.0	81	2	Q71J19_MACFA	Q71J19 macaca fasc						
118	20	100.0	81	2	Q6ESF6_ORYSA	Q6ESF6 oryza sativ						
119	20	100.0	81	2	Q6HR28_BACAN	Q6HR28 bacillus an						
120	20	100.0	81	2	Q92U02_RHIME	Q92U02 rhizobium m						
121	20	100.0	81	2	Q7ZT96_CARAU	Q7ZT96 carassius a						
122	20	100.0	82	2	Q4VXZ3_HUMAN	Q4VXZ3 homo sapien						
123	20	100.0	82	2	Q4R805_MACFA	Q4R805 macaca fasc						
124	20	100.0	82	2	Q775D9_9CAUD	Q775D9 bordetella						
125	20	100.0	82	2	Q5L1Y9_GEOXA	Q5L1Y9 geobacillus						
126	20	100.0	82	2	Q5WK37_BACSK	Q5WK37 bacillus cl						
127	20	100.0	82	2	Q8PRN4_XANAC	Q8PRN4 xanthomonas						
128	20	100.0	82	2	Q4SZT2_TETNG	Q4SZT2 tetraodon n						
129	20	100.0	83	1	Y46S_SYNY3	P73882 synectocyst						
130	20	100.0	83	2	Q775E0_9CAUD	Q775E0 bordetella						
131	20	100.0	83	2	Q8NRT6_CORGL	Q8NRT6 corynebacte						
132	20	100.0	84	2	Q85FW9_9CAUD	Q85FW9 mycobacteri						
133	20	100.0	84	2	Q4JXP2_CORJK	Q4JXP2 corynebacte						
134	20	100.0	84	2	Q9S1X4_STRCO	Q9S1X4 streptomyc						
135	20	100.0	85	2	Q42921_SCHPO	Q42921 schizosacch						
136	20	100.0	85	2	Q7QSD1_GIALA	Q7QSD1 giardia lam						
137	20	100.0	85	2	Q9XHX2_CABEL	Q9XHX2 caenorhabdi						
138	20	100.0	85	2	Q7U6H4_SYNFX	Q7U6H4 synecococc						
139	20	100.0	86	1	GBG_NEUCR	Q7RWT0 neurospora						
140	20	100.0	87	2	Q9MY39_HUMAN	Q9MY39 homo sapien						
141	20	100.0	88	1	Y2638_BACHD	Q9K9K7 bacillus ha						
142	20	100.0	88	2	Q5JGVS_PYKRO	Q5JGVS pyrococcus						
143	20	100.0	88	2	Q58MT8_9CAUD	Q58MT8 cyanophage						
144	20	100.0	88	2	Q5SLG1_THETB	Q5SLG1 thermus the						
145	20	100.0	88	2	Q72H44_THET2	Q72H44 thermus the						
146	20	100.0	88	2	Q8RA16_THETN	Q8RA16 thermoanaer						
147	20	100.0	88	2	Q8END8_OCEIH	Q8END8 oceanobacil						
148	20	100.0	89	2	Q9BCW5_HUMAN	Q9BCW5 homo sapien						
149	20	100.0	89	2	Q9GIZ7_HUMAN	Q9GIZ7 homo sapien						
150	20	100.0	89	2	Q9GJ10_HUMAN	Q9GJ10 homo sapien						
ALIGNMENTS												
RESULT 1												
Q89492_9BROM												
ID	Q89492_9BROM	PRELIMINARY;	PRT;	27 AA.								
AC	Q89492_9BROM											
DT	01-NOV-1996	(TrEMBLrel. 01, Created)										
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)										
DT	01-FEB-2005	(TrEMBLrel. 29, Last annotation update)										
DE	ORF 1.											
OS	Cucumber mosaic virus (cucumber mosaic cucumovirus).											
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;											
OC	Cucumovirus.											
OX	NCBI_TaxID=12305;											
RN	[1]											
RP	NUCLEOTIDE SEQUENCE.											
RX	MEDLINE=88179532; PubMed=3354198;											
RA	Kaper J.M., Tounignant M.E., Steen M.T.;											
RT	"Cucumber mosaic virus-associated RNA 5: XI. Comparison of 14 CARNA 5											
RT	variants relates ability to induce tomato necrosis to a conserved											
RT	nucleotide sequence."											
RL	Virology 163:284-292(1988).											
DR	EMBL; M20357; AAA46403.1; -; Genomic_RNA.											
DR	EMBL; M20350; AAA46385.1; -; Genomic_RNA.											
DR	EMBL; M20352; AAA46398.1; -; Genomic_RNA.											
DR	EMBL; M20353; AAA46391.1; -; Genomic_RNA.											
DR	EMBL; M20354; AAA46394.1; -; Genomic_RNA.											
DR	EMBL; M20355; AAA46397.1; -; Genomic_DNA.											
DR	EMBL; M20356; AAA46400.1; -; Genomic_RNA.											
DR	PIR; JEO015; JEO015.											
DR	PIR; JS0104; JS0104.											
SQ	SEQUENCE	27 AA;	2827 MW;	BC60426D890A5E9A	CRC64;							
Query Match												
Best Local Similarity												
Matches												
4; Conservative												
0; Mismatches												
0; Indels												
0; Gaps												
QY	1	REDL 4										
Db	11	REDL 14										
RESULT 2												
Q86LN9_9METZ												
ID	Q86LN9_9METZ	PRELIMINARY;	PRT;	29 AA.								
AC	Q86LN9_9METZ											
DT	01-JUN-2003	(TrEMBLrel. 24, Created)										
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)										
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)										
DE	Paired-type homeodomain-containing protein (Fragment).											
OS	Spongilla sp. SL-2003.											
OC	Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;											
OC	Haploeclerida; Spongillidae; Spongilla.											
RN	NCBI_TaxID=220381;											
RP	NUCLEOTIDE SEQUENCE.											
RA	Lee S.E., Gates R.D., Jacobs D.K.;											
RT	"Gene Fishing: the use of a simple protocol to isolate multiple											
RT	homeodomain classes from diverse invertebrate taxa."											
RL	J. Mol. Evol. 0:0-0(2003).											
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).											
DR	EMBL; AY187697; AA045637.1; -; Genomic_DNA.											
DR	GO; GO:0005634; C:nucleus; IEA.											
DR	GO; GO:0003700; F:transcription factor activity; IEA.											
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.											
DR	InterPro; IPR001356; Homeobox.											
DR	Pfam; PF00046; Homeobox; 1.											
DR	PRINTS; PR00024; HOMEBOX.											
DR	ProDom; PD000010; Homeobox; 1.											
DR	DNA-binding; Homeobox; Nuclear protein.											
KW	NON_TER	1										
FT	NON_TER	29										
SQ	SEQUENCE	29 AA;	3393 MW;	3B7DC4820DA3E4E9	CRC64;							
Query Match												
Best Local Similarity												
Matches												
4; Conservative												
0; Mismatches												
0; Indels												
0; Gaps												
QY	1	REDL 4										
Db	14	REDL 17										
RESULT 3												
Q4YFAB_PLABE												
ID	Q4YFAB_PLABE	PRELIMINARY;	PRT;	30 AA.								
AC	Q4YFAB_PLABE											
DT	13-SEP-2005	(TrEMBLrel. 31, Created)										
DT	13-SEP-2005	(TrEMBLrel. 31, Last sequence update)										
DT	13-SEP-2005	(TrEMBLrel. 31, Last annotation update)										
DE	Hypothetical protein (Fragment).											
GN	ORFNames=PB404646.00.0;											
OS	Plasmodium berghei.											
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.											
OX	NCBI_TaxID=5821;											
RN	[1]											
RP	NUCLEOTIDE SEQUENCE.											

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CA01005700; CA103310.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 30 AA; 3559 MW; 3565280356933DA8 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 4
Q4KA34_PSEFS
ID Q4KA34_PSEFS PRELIMINARY; PRT; 31 AA.
AC Q4KA34;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PFL_3799;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
RA PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavris D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY93062.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 31 AA; 3593 MW; 45D45B4E6AE51501 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 13 REDL 16

RESULT 5
Q86LP0_9METZ
ID Q86LP0_9METZ PRELIMINARY; PRT; 32 AA.
AC Q86LP0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Paired-type homeodomain-containing protein (Fragment).
OS Acarnus sp. SL-2003.

OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Poecilosclerida; Myxillina; Myxillidae; Acarnus.
OX NCBI_TaxID=220380;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee S.E., Gates R.D., Jacobs D.K.;
RT "Gene Fishing: the use of a simple protocol to isolate multiple
RT homeodomain classes from diverse invertebrate taxa.";
RL J. Mol. Evol. 0:0-0(2003).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AY187696; AAC45636.1; -; Genomic_DNA.
DR HSSP; P06601; 1FJL.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
FT NON TER 32 32
SQ SEQUENCE 32 AA; 3813 MW; 85872CAB6884930D CRC64;

Query Match 100.0%; Score 20; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 14 REDL 17

RESULT 6
Q95LA6_PIG
ID Q95LA6_PIG PRELIMINARY; PRT; 34 AA.
AC Q95LA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LIM homeodomain protein 3b (Fragment).
GN Name=Lhx3;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21453325; PubMed=11470784; DOI=10.1074/jbc.M103888200;
RA Sloop K.W., Dwyer C.J., Rhodes S.J.;
RT "An isoform-specific inhibitory domain regulates the LHX3 LIM
RT homeodomain factor holoprotein and the production of a functional
RT alternate translation form.";
RL J. Biol. Chem. 276:36311-36319(2001).
DR EMBL; AF370445; AAL09570.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON TER 34 34
SQ SEQUENCE 34 AA; 3748 MW; 7083C3258F8E414C CRC64;

Query Match 100.0%; Score 20; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 26 REDL 29

RESULT 7

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Q9UQY7 TRAVE
ID Q9UQY7 TRAVE PRELIMINARY; PRT; 35 AA.
AC Q9UQY7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Lignin peroxidase isoenzyme TVLP15 (Fragment).
OS Trametes versicolor (White-rot fungus) (Coriolus versicolor).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=5325;
RN [1]
RP PROTEIN SEQUENCE. PubMed=8424691; DOI=10.1006/abbi.1993.1008;
RX MEDLINE=9343365; Wellinder K.G., Nyman P.O.;
RA Johansson T., Wellinder K.G., Nyman P.O.;
RT "Isozymes of lignin peroxidase and manganese(II) peroxidase from the
white-rot basidiomycete Trametes versicolor. II. Partial sequences,
peptide maps, and amino acid and carbohydrate compositions."
RL Arch. Biochem. Biophys. 300:57-62(1993).
DR PIR; S29728; S29728.
DR HSSP; P11542; IQPA.
SQ SEQUENCE 35 AA; 3680 MW; B497C9618EC1FDD7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 22 REDL 25

RESULT 8
Q570E3 ARATH
ID Q570E3 ARATH PRELIMINARY; PRT; 35 AA.
AC Q570E3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Tubulin alpha-2/alpha-4 chain (Fragment).
GN Name=At1g04820;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Toki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK220765; BAD3966.1; -; mRNA.
FT NON TER 1
FT SEQUENCE 35 AA; 3941 MW; BA65FC4A2584DA9C CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 7 REDL 10

RESULT 9
Q5NQJ6 ZYMO
ID Q5NQJ6 ZYMO PRELIMINARY; PRT; 35 AA.
AC Q5NQJ6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)

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DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=ZMO0384;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=15592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.-S., Yoon K.-O., Jung C., Kim J.-J.,
RA Hong J.-H., Kim J.-H., Kil J.-I., Park C.-J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y.,
RA Kang H.-L., Lee S.-Y., Lee K.-J., Kang H.-S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
ZM4."
RL Nat. Biotechnol. 23:63-68(2005).
DR EMBL; AE008692; AAV89008.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 35 AA; 3855 MW; 51DC67425C928BBE CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 17 REDL 20

RESULT 10
Q9QW57 9MURI
ID Q9QW57 9MURI PRELIMINARY; PRT; 36 AA.
AC Q9QW57;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HES-1=HOMEODOMAIN protein.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93087202; PubMed=1360650;
RA Thomas P.O., Rathjen P.D.;
RT "HES-1, a novel homeobox gene expressed by murine embryonic stem
cells, identifies a new class of homeobox genes."
RL Nucleic Acids Res. 20:5840-5840(1992).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR01356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00046; Homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS50071; HOMEBOX2; 1.
KW DNA-binding; Homeobox; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 36 AA; 4262 MW; AEB316C35D10CC13 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 23 REDL 26

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RESULT 11
 Q56Y22 ARATH PRELIMINARY; PRT; 38 AA.
 AC Q56Y22;
 DT 10-MAY-2005 (TRENBLrel. 30, Created)
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
 DE Tubulin alpha-2/alpha-4 chain.
 GN Name=Atlg04820;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tokoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
 RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK221178; BAD95252.1; -; mRNA.
 SQ SEQUENCE 38 AA; 4258 MW; 2365FF71BC99EFF5 CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 10 REDL 13

RESULT 12
 O19688 HUMAN PRELIMINARY; PRT; 39 AA.
 AC O19688;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE HLA-B*27 variant exon 2 (Alpha domain) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Blaszyk R., Weber M., Salama A.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X83727; CAA58698.1; -; Genomic DNA.
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019882; P:antigen presentation; IEA.
 DR InterPro; IPR001039; MHC_alpha_A1A2.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD009050; MHC_I; 1.
 FT NON TER 1
 FT NON TER 39
 SQ SEQUENCE 39 AA; 4748 MW; F5E3FD2A53138908 CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 24 REDL 27

RESULT 13
 O61645 APLCA PRELIMINARY; PRT; 39 AA.
 AC O61645;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Alpha-tubulin (Fragment).
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;
 OC Aplysioidae; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sung Y.J., Zhu D.F., Ambron R.T.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF055329; AAC12647.1; -; mRNA.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002452; Alpha_tubulin.
 DR PANTHER; PTHR11588:SP1; Alpha_tubulin; 1.
 FT NON TER 1
 FT NON TER 39
 SQ SEQUENCE 39 AA; 4393 MW; 0D3A0EB30DFC29AF CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 9 REDL 12

RESULT 14
 Q8MTM6_9DIPT PRELIMINARY; PRT; 39 AA.
 AC Q8MTM6;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE EIF5A (Fragment).
 OS Culicoides sonorensis.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
 OC Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
 OX NCBI_TaxID=179676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=22309032; PubMed=12421417;
 RA Campbell C.L., Wilson W.C.;
 RT "Differentially expressed midgut transcripts in Culicoides sonorensis
 (Diptera: ceratopogonidae) following Orbivirus (reoviridae) oral
 feeding.";
 RL Insect Mol. Biol. 11:595-604 (2002).
 DR EMBL; AY095267; AM28346.1; -; mRNA.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006413; P:translational initiation; IEA.
 DR InterPro; IPR001884; EIF5A_hypusine.
 DR Pfam; PF01287; eIF-5a; 1.
 FT NON TER 1
 FT NON TER 39
 SQ SEQUENCE 39 AA; 4461 MW; 0C68CB2813C539D3 CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 REDL 4
 Db 28 REDL 31

RESULT 15		Query Match	100.0%;	Score 20;	DB 2;	Length 41;
Q74264_9HIV1		Best Local Similarity	100.0%;	Pred. No. 1e+03;	0;	Indels 0;
ID Q74264_9HIV1 PRELIMINARY;		Matches	4;	Conservative	0;	Mismatches 0;
AC Q74264;						Gaps 0;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)						
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)						
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)						
DE Reverse transcriptase (Fragment).						
GN Name:pol;						
OS Human immunodeficiency virus 1.						
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;						
OC Primate lentivirus group.						
OC NCBI_TaxID=11676;						
RN [1]						
RP NUCLEOTIDE SEQUENCE.						
RX MEDLINE=97000986; PubMed=8844016;						
RA Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;						
RT "Point mutant frequencies in the pol gene of human immunodeficiency						
RT virus type 1 are two- to threefold lower than those of env.";						
RL AIDS Res. Hum. Retroviruses 12:1117-1128(1996).						
RN [2]						
RP NUCLEOTIDE SEQUENCE.						
RX MEDLINE=95074869; PubMed=7983713;						
RA Najera I., Holguin A., Quinones-Mateu M.E., Munoz-Fernandez M.A.,						
RA Najera R., Lopez-Galindez C., Domingo E.;						
RT "Pol gene quasiespecies of human immunodeficiency virus: mutations						
RT associated with drug resistance in virus from patients undergoing no						
RT drug therapy.";						
RL J. Virol. 69:23-31(1995).						
DR EMBL; U14893; AAC55799.1; -; Genomic_DNA.						
DR GO; GO:0003723; F:RNA binding; IEA.						
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.						
DR GO; GO:0016740; F:transferase activity; IEA.						
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.						
DR InterPro: IPR000477; RVTse.						
KW RNA-directed DNA polymerase.						
FT NON_TER 1						
FT NON_TER 39						
SQ SEQUENCE 39 AA; 4754 MW; 487862AD9E905DAF CRC64;						
Query Match		100.0%;	Score 20;	DB 2;	Length 39;	
Best Local Similarity		100.0%;	Pred. No. 9.8e+02;			
Matches		4;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps						
QY 1 REDL 4						
Db						
22 REDL 25						
RESULT 16						
Q9UW29_9PEZI						
ID Q9UW29_9PEZI PRELIMINARY;						
AC Q9UW29;						
DT 01-MAY-2000 (TrEMBLrel. 13, Created)						
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)						
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)						
DE MAT-2 HMG box protein (Fragment).						
OS Ceratocystis pinicola.						
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;						
OC Hypocremycetidae; Microascales; Microascales incertae sedis;						
OC Ceratocystis.						
OX NCBI_TaxID=72031;						
RN [1]						
RP NUCLEOTIDE SEQUENCE.						
RC STRAIN=C795;						
RA Withuhn R., Harrington T., Steimel J., Wingfield B., Wingfield M.;						
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.						
DR EMBL; AF164194; AAD48810.1; -; Genomic_DNA.						
FT NON_TER 1						
FT NON_TER 41						
SQ SEQUENCE 41 AA; 4848 MW; 6A29093D521ADC59 CRC64;						
Query Match		100.0%;	Score 20;	DB 2;	Length 41;	
Best Local Similarity		100.0%;	Pred. No. 1e+03;			
Matches		4;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps						
QY 1 REDL 4						
Db						
22 REDL 25						
RESULT 17						
Q8CH67_MOUSE						
ID Q8CH67_MOUSE PRELIMINARY;						
AC Q8CH67;						
DT 01-MAR-2003 (TrEMBLrel. 23, Created)						
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)						
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)						
DE Eukaryotic initiation factor 5A isoform II (Fragment).						
GN Names:Elf5a2;						
GN Mus musculus (Mouse).						
OS Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Eukaryota; Metazoa; Euarchoptogilres; Glires; Rodentia; Sciurognathi;						
OC Muridae; Murinae; Mus.						
OX NCBI_TaxID=10090;						
RN [1]						
RP NUCLEOTIDE SEQUENCE.						
RC STRAIN=BALB/c;						
RX MEDLINE=21100881; PubMed=11161802; DOI=10.1006/geno.2000.6418;						
RA Jenkins Z.A., Haag P.G., Johansson H.E.;						
RT "Human eIF5A2 on chromosome 3q25-q27 is a phylogenetically conserved						
RT vertebrate variant of eukaryotic translation initiation factor 5A with						
RT tissue-specific expression.";						
RL Genomics 71:101-109(2001).						
RN [2]						
RP NUCLEOTIDE SEQUENCE.						
RC STRAIN=BALB/c;						
RA Jenkins Z.A., Haag P.G., Johansson H.E.;						
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.						
DR EMBL; AF377869; AA017899.1; -; Genomic_DNA.						
DR GO; GO:0003743; P:translation initiation factor activity; IEA.						
DR GO; GO:0006413; P:translational initiation; IEA.						
DR InterPro: IPR001884; EIF5A_hypusine.						
DR Pfam; PF01287; eIF-5a; 1.						
KW Initiation factor.						
FT NON_TER 1						
FT NON_TER 41						
SQ SEQUENCE 41 AA; 4438 MW; E27B44C07A1C9622 CRC64;						
Query Match		100.0%;	Score 20;	DB 2;	Length 41;	
Best Local Similarity		100.0%;	Pred. No. 1e+03;			
Matches		4;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps						
QY 1 REDL 4						
Db						
10 REDL 13						
RESULT 18						
Q8WMC5_PONPY						
ID Q8WMC5_PONPY PRELIMINARY;						
AC Q8WMC5;						
DT 01-MAR-2002 (TrEMBLrel. 20, Created)						
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)						
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)						
DE NP1P-like protein (Fragment).						
OS Pongo pygmaeus (Orangutan).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;						
OC Pongo.						
OX NCBI_TaxID=9600;						
RN [1]						
RP NUCLEOTIDE SEQUENCE.						
RX MEDLINE=21470411; PubMed=11586358; DOI=10.1038/35097067;						
RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,						

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RA Rocchi M., Eichler E.E.;
RT "Positive selection of a gene family during the emergence of humans
RL Nature 413:514-519(2001).
RL EMBL; AF364210; AAL50437.1; -; Genomic_DNA.
DR EMBL; AF364215; AAL50447.1; -; Genomic_DNA.
DR InterPro; IPR009443; NPIP.
DR Pfam; PF06409; NPIP; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5332 MW; EEB122D84370E988 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db |||| 5 REDL 8

RESULT 19
Q8WN16_HYLKL PRELIMINARY; PRT; 45 AA.
AC Q8WN16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NPIP-like protein (Fragment).
OS Hylobates klossii (Kloss's gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Hylobatidae; Hylobates.
OC NCBI_TaxID=9587;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21470411; PubMed=11586358; DOI=10.1038/35097067;
RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,
RA Rocchi M., Eichler E.E.;
RT "Positive selection of a gene family during the emergence of humans
RL Nature 413:514-519(2001).
RL EMBL; AF364217; AAL50451.1; -; Genomic_DNA.
DR InterPro; IPR009443; NPIP.
DR Pfam; PF06409; NPIP; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5404 MW; EEB294384370E988 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db |||| 5 REDL 8

RESULT 20
Q84U35_9ASPA PRELIMINARY; PRT; 45 AA.
AC Q84U35;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB19 (Fragment).
GN Name=MYB19;
OS Dendrobium sp. XWV-2002-19.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendroblinae;
OC Dendrobium.
OC NCBI_TaxID=217465;
```

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RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22661209; PubMed=12777054; DOI=10.1023/A:1023050110077;
RA Wu X.-M., Lim S.-H., Yang W.-C.;
RT "Characterization, expression and phylogenetic study of R2R3-MYB genes
in orchid.";
RL Plant Mol. Biol. 51:959-972(2003).
DR EMBL; AF485910; AAO49428.1; -; mRNA.
DR HSSP; P06876; 1GV2.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb_DNA_bd.
DR PROSITE; PS50090; MYB_3; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5286 MW; E7348A72534C36C9 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db |||| 8 REDL 11

RESULT 21
Q9GT46_ANOGA PRELIMINARY; PRT; 46 AA.
AC Q9GT46;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ribosomal protein S18 (Fragment).
GN Name=IrpS18;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OC NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=G3;
RC MEDLINE=20481919; PubMed=11005829; DOI=10.1073/pnas.180060997;
RA Oduol F., Xu J., Niare O., Natarajan R., Vernick K.D.;
RT "Genes identified by an expression screen of the vector mosquito
Anopheles gambiae display differential molecular immune response to
malaria parasites and bacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:11397-11402(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G3;
RA Oduol F.O., Xu J., Niare O., Natarajan R., Vernick K.D.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein S13p family.
DR EMBL; AF283268; AAC15373.1; -; mRNA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001892; Ribosomal_S13.
DR Pfam; PF00416; Ribosomal_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13_1; 1.
DR PROSITE; PS0159; RIBOSOMAL_S13_2; 1.
KW Ribonucleoprotein; Ribosomal protein.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5519 MW; 0B91AEB7D54EFA85 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

DR TIGR; PSPT03546; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 47 AA; 5258 MW; 935E23600334F315 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 2 REDL 5

RESULT 22
Q8WNH3_CERAE PRELIMINARY; PRT; 46 AA.

ID Q8WNH3_CERAE PRELIMINARY; PRT; 46 AA.
AC Q8WNH3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NP1P-like protein (Fragment).
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21470411; PubMed=11586358; DOI=10.1038/35097067;
RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,
RA Rocchi M., Eichler E.E.;
RT "Positive selection of a gene family during the emergence of humans
RT and African apes";
RL Nature 413:514-519(2001).
DR EMBL; AF364227; AAL50471.1; -; Genomic_DNA.
DR InterPro; IPR009443; NP1P.
DR Pfam; PF06409; NP1P; 1.
FT NON_TER 1
FT TER 46
SQ SEQUENCE 46 AA; 5429 MW; E552A244F6B0A333 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
|||
Db 5 REDL 8

RESULT 23
Q87Z84_PSESM PRELIMINARY; PRT; 47 AA.

ID Q87Z84_PSESM PRELIMINARY; PRT; 47 AA.
AC Q87Z84;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PSPT03546;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=DC3000;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
DR EMBL; AE016853; AA057021.1; -; Genomic DNA.

DR GO; GO:0042612; C:MHC class I protein complex; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019882; P:antigen presentation; IEA.
 DR InterPro; IPR001039; MHC_I_alpha_A1A2.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 FT NON_TER 1
 FT NON_TER 49
 SQ SEQUENCE 49 AA; 5983 MW; BDFE863415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 42 REDL 45

RESULT 26

ID Q7YQ55 PHOSS PRELIMINARY; PRT; 49 AA.
 AC Q7YQ55
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MHC class I antigen alpha 1 subunit (Fragment).
 GN Name=Phsi;
 OS Phocoena sinus (Vaquita).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Phocoenidae; Phocoena.
 OX NCBI_TaxID=42100;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Munguia-Vega A.; Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
 RA Rojas-Bracho L.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY170895; AA017683.1; -; Genomic_DNA.
 DR SMR; Q7YQ55; 1-49.
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR InterPro; IPR001039; MHC_I_alpha_A1A2.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 FT NON_TER 1
 FT NON_TER 49
 SQ SEQUENCE 49 AA; 6010 MW; BDFE94A415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 42 REDL 45

RESULT 27

ID Q7YQ56 PHOSS PRELIMINARY; PRT; 49 AA.
 AC Q7YQ56
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MHC class I antigen alpha 1 subunit (Fragment).

GN Name=Phsi;
 OS Phocoena sinus (Vaquita).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Phocoenidae; Phocoena.
 OX NCBI_TaxID=42100;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Munguia-Vega A.; Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
 RA Rojas-Bracho L.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY170894; AA017682.1; -; Genomic_DNA.
 DR SMR; Q7YQ56; 1-49.
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019882; P:antigen presentation; IEA.
 DR InterPro; IPR001039; MHC_I_alpha_A1A2.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 FT NON_TER 1
 FT NON_TER 49
 SQ SEQUENCE 49 AA; 5953 MW; AFCEA53415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
 Db 42 REDL 45

RESULT 28

ID Q7YQ57 PHOSS PRELIMINARY; PRT; 49 AA.
 AC Q7YQ57
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MHC class I antigen alpha 1 subunit (Fragment).
 GN Name=Phsi;
 OS Phocoena sinus (Vaquita).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Phocoenidae; Phocoena.
 OX NCBI_TaxID=42100;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Munguia-Vega A.; Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
 RA Rojas-Bracho L.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY170893; AA017681.1; -; Genomic_DNA.
 DR SMR; Q7YQ57; 1-49.
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019882; P:antigen presentation; IEA.
 DR InterPro; IPR001039; MHC_I_alpha_A1A2.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 FT NON_TER 1
 FT NON_TER 49

```

SQ SEQUENCE 49 AA; 5983 MW; BDFE863415FF2B5B CRC64;
Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 42 REDL 45

RESULT 29
Q7YQ58 PHOSS
ID Q7YQ58 PHOSS PRELIMINARY; PRT; 49 AA.
AC Q7YQ58;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE MHC class I antigen alpha 1 subunit (Fragment).
GN Name=Phsi;
OS Phocoena sinus (Vaquita).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=42100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A.;
RT "Study of the major histocompatibility complex in the evolutionary and
demographic history of the porpoise (Phocoena sinus).";
Thesis (2003), CIBNOR, La Paz, BCS, Mexico, In press.
[2]
RA NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A., Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
Rojas-Bracho L.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170891; AA017679.1; -; Genomic_DNA.
DR SMR; Q7YQ59; 1-49.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_A1A2.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5954 MW; BDFE8634128F5C5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 42 REDL 45

RESULT 31
Q7YQ60 PHOSS
ID Q7YQ60 PHOSS PRELIMINARY; PRT; 49 AA.
AC Q7YQ60;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE MHC class I antigen alpha 1 subunit (Fragment).
GN Name=Phsi;
OS Phocoena sinus (Vaquita).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=42100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A.;
RT "Study of the major histocompatibility complex in the evolutionary and
demographic history of the porpoise (Phocoena sinus).";
Thesis (2003), CIBNOR, La Paz, BCS, Mexico, In press.
[2]
RA NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A., Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
Rojas-Bracho L.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170890; AA017678.1; -; Genomic_DNA.
DR SMR; Q7YQ60; 1-49.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_A1A2.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5983 MW; BDFE863415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 42 REDL 45

RESULT 30
Q7YQ59 PHOSS
ID Q7YQ59 PHOSS PRELIMINARY; PRT; 49 AA.
AC Q7YQ59;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE MHC class I antigen alpha 1 subunit (Fragment).
GN Name=Phsi;
OS Phocoena sinus (Vaquita).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=42100;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

Db          42 REDL 45

RESULT 32
Q4ZR70_PSESY PRELIMINARY; PRT; 49 AA.
AC Q4ZR70;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Psyr_3320;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
RA Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
RA Land M., Richardson P.M., Kyripides N.C., Ivanova N.;
RA "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RN Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Feil H., Feil W.S., Lindow S.E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000075; AAY38352.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5403 MW; 2989483E23600334 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 7 REDL 10

RESULT 33
TBA_BLEVA
ID TBA_BLEVA STANDARD; PRT; 50 AA.
AC Q08628;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tubulin alpha chain (Fragment).
OS Blepharisma japonicum.
OC Eukaryota; Alveolata; Ciliophora; Heterotriches; Heterotrichida;
OC Blepharismidae; Blepharisma.
OX NCBI_TaxID=5961;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9328144; PubMed=7685500;
RA Liang A., Heckmann K.;
RT "Blepharisma uses UAA as a termination codon.";
RL Naturwissenschaften 80:225-226(1993).
CC -!- FUNCTION: Tubulin is the major constituent of microtubules. It
CC binds two moles of GTP, one at an exchangeable site on the beta
CC chain and one at a nonexchangeable site on the alpha-chain.
CC -!- SUBUNIT: Dimer of alpha and beta chains.
CC -!- SIMILARITY: Belongs to the tubulin family.

```

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; S62518; AAB27144.1; -; mRNA.
DR PIR; S36687; S36687.
DR InterPro; IPR002452; Alpha tubulin.
DR InterPro; IPR000217; Tubulin.
DR PANTHER; PTHR11588:SF1; Alpha tubulin; 1.
DR PANTHER; PTHR11588; Tubulin; 1.
DR PROSITE; PS00227; TUBULIN; PARTIAL.
KW GTP-binding; Microtubule; Nucleotide-binding.
FT NON TER 1
SQ SEQUENCE 50 AA; 5659 MW; 3749548FCEA9E3F9 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 19 REDL 22

RESULT 34
Q4X611_PLACH PRELIMINARY; PRT; 50 AA.
ID Q4X611;
AC Q4X611;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC302493.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ribosomal protein S13P family.
DR EMBL; CAATJ01009502; CAH87495.1; -; Genomic_DNA.
DR InterPro; IPR001892; Ribosomal S13.
DR ProDom; PD001363; Ribosomal S13.
DR PROSITE; PS00646; RIBOSOMAL_S13_1; 1.
DR PROSITE; PS0159; RIBOSOMAL_S13_2; 1.
KW Hypothetical protein; Ribonucleoprotein; Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 50 AA; 5889 MW; DE05635A6A3419ED CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 4 REDL 7

RESULT 35
Q7ZT89_CARAU

```

Query Match	100.0%;	Score 20;	DB 2;	Length 51;
Best Local Similarity	100.0%;	Pred. No. 1.3e+03;		

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 7 REDL 10

RESULT 39

Q8MZQ7_9DIPT
ID Q8MZQ7_9DIPT PRELIMINARY; PRT; 52 AA.
AC Q8MZQ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome P450 (Fragment).
GN Name=Cyp4C3;
OS Drosophila pachea.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=103846;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Azadan R.J., Danielson P.B., Fogleman J.C.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506532; AAM27400.1; -; mRNA.
DR FlyBase; FBgn0062760; DpacCyp4C3.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
FT NON_TER 1
SQ SEQUENCE 52 AA; 6072 MW; 9EDE3D761CEFF7DD6 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 27 REDL 30

RESULT 40

Q58LK4_9CAUD
ID Q58LK4_9CAUD PRELIMINARY; PRT; 52 AA.
AC Q58LK4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PSSM4_094;
OS Cyanophage P-SSM4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=268747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15828858; DOI=10.1371/journal.pbio.0030144;
RA Sullivan M.B., Coleman M.L., Weigle P., Rohwer F., Chisholm S.W.;
RT "Three prochlorococcus cyanophage genomes: signature features and
ecological interpretations.";
RL PLoS Biol. 3:E144-E144 (2005).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RA Lindell D., Sullivan M.B., Johnson Z.I., Tolonen A., Rohwer F.,
RA Chisholm S.W.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY940168; AAX46895.1; -; Genomic_DNA.
KW Hypothetical protein.

SQ SEQUENCE 52 AA; 6163 MW; 7AF8852AF1933EB0 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 33 REDL 36

RESULT 41

Q5XYZ2_BORGA
ID Q5XYZ2_BORGA PRELIMINARY; PRT; 52 AA.
AC Q5XYZ2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=EGP139;
OS Borrelia garinii PBI.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxID=290434;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PBI;
RA Glockner G., Lehmann R., Romualdi A., Pradella S.,
RA Schulte-Spechtel U., Schilhabel M., Wilske B., Sühnel J., Platzner M.;
RT "Comparative analysis of the Borrelia garinii genome.";
RN Nucleic Acids Res. 32:6038-6046(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PBI;
RA Gloeckner G., Schilhabel M., Lehmann R., Platzner M.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY729222; AAU85990.1; -; Genomic_DNA.
KW Hypothetical protein.

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
|||||
Db 13 REDL 16

RESULT 42

Q96XL7_SULTO
ID Q96XL7_SULTO PRELIMINARY; PRT; 54 AA.
AC Q96XL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 54aa long hypothetical transcription factor.
GN OrderedLocustNames=ST2500.1; ORFNames=STS247;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OX NCBI_TaxID=111955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yanagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; BA000023; BAB67610.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 54 AA; 6380 MW; E9D0637C4204B5F4 CRC64;

Query Match		100.0%;	Score 20;	DB 2;	Length 54;
Best Local Similarity		100.0%;	Pred. No. 1.4e+03;		
Matches		4;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 REDL 4				
DB	17 REDL 20				
RESULT 43					
ID	Q9GLJ2_PIG	PRELIMINARY;	PRT;	54 AA.	
AC	Q9GLJ2;				
DT	01-MAR-2001 (TrEMBLrel. 16, Created)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	DNA-PK interaction-like protein (Fragment).				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;				
OC	Sub.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Smith T.P.L., Fahrrenkrug S.C., Rohrer G.A., Simmen F.A.,				
RA	Rexroad C.E. III, Keefe J.W.;				
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF267715; AAG25931.1; -; Genomic_DNA.				
DR	HSPB; Q99828; 1DGU.				
DR	SMR; Q9GLJ2; 1-54.				
DR	GO; GO:0005509; F:calcium ion binding; IEA.				
DR	InterPro; IPR002048; EF-hand.				
DR	Pfam; PF00036; efhand; 1.				
DR	PROSITE; PS00012; EF-hand; 1.				
DR	PROSITE; PS00018; EF-HAND; UNKNOWN_1.				
FT	NON TER 1				
FT	NON TER 54				
FT	NON TER 54				
SQ	SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;				
Query Match					
Best Local Similarity		100.0%;	Score 20;	DB 2;	Length 54;
Matches		4;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 REDL 4				
DB	24 REDL 27				
RESULT 44					
ID	Q94KJ8_PINTA	PRELIMINARY;	PRT;	54 AA.	
AC	Q94KJ8;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Alpha-tubulin (Fragment).				
OS	Pinus taeda (loblolly pine).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.				
OX	NCBI_TaxID=3352;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Lorenz W.W., Dean J.F.D.;				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF357237; AAK49527.1; -; mRNA.				
DR	GO; GO:0005874; C:microtubule; IEA.				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	GO; GO:0007018; F:microtubule-based movement; IEA.				
DR	InterPro; IPR002452; Alpha_tubulin.				
FT	PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.				
FT	NON TER 1				
FT	NON TER 1				
SQ	SEQUENCE 54 AA; 6111 MW; 2A980A49B95A84A5 CRC64;				
Query Match					
Best Local Similarity		100.0%;	Score 20;	DB 2;	Length 54;
Matches		4;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 REDL 4				
DB	24 REDL 27				
RESULT 45					
ID	O69433_9BACI	PRELIMINARY;	PRT;	54 AA.	
AC	O69433;				
DT	01-AUG-1998 (TrEMBLrel. 07, Created)				
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	TnpA protein (Fragment).				
GN	Name=tnpA;				
OS	Exiguobacterium sp.				
OC	Bacteria; Firmicutes; Bacilliales; Bacillaceae; Exiguobacterium.				
OX	NCBI_TaxID=44751;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=TC38-2b;				
RX	MEDLINE=98195721; PubMed=9534232;				
RA	Bogdanova E.S., Bass I.A., Minakhin L.S., Petrova M.A., Mindlin S.Z.,				
RA	Volodin A.A., Kalyaeva E.S., Tiedge G.M., Hobman J.L., Brown N.L.,				
RA	Nikifirov V.G.;				
RT	"horizontal spread of mer operons among Gram-positive bacteria in				
RT	natural environments.";				
RL	Microbiology 144:609-620 (1998).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=TC38-2b;				
RA	Minakhin L.;				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; Y08064; CAA69303.1; -; Genomic_DNA.				
DR	GO; GO:0003677; F:DNA binding; IEA.				
DR	GO; GO:0004803; F:transposase activity; IEA.				
DR	GO; GO:0006313; P:DNA transposition; IEA.				
DR	InterPro; IPR002513; Transposase_7.				
DR	Pfam; PF01526; Transposase_7; 1.				
FT	NON TER 1				
FT	NON TER 1				
SQ	SEQUENCE 54 AA; 6229 MW; 8939739E0F0D4803 CRC64;				
Query Match					
Best Local Similarity		100.0%;	Score 20;	DB 2;	Length 54;
Matches		4;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 REDL 4				
DB	15 REDL 18				
RESULT 46					
ID	O69233_BACCE	PRELIMINARY;	PRT;	54 AA.	
AC	O69233;				
DT	01-AUG-1998 (TrEMBLrel. 07, Created)				
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)				
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)				
DE	TnpA protein (Transposase) (Fragment).				
GN	Name=tnpA;				
OS	Bacillus cereus.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;				
OC	Bacillus cereus group.				
OX	NCBI_TaxID=11396;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=RC607.				
RX	MEDLINE=98195721; PubMed=9534232;				
RA	Bogdanova E.S., Bass I.A., Minakhin L.S., Petrova M.A., Mindlin S.Z.,				

RA Volodin A.A., Kalyaeva E.S., Tiedge G.M., Hobman J.L., Brown N.L.,
RA Nifkifirov V.G.;
RT "Horizontal spread of mer operons among Gram-positive bacteria in
RT natural environments.";
RL Microbiology 144:609-620(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RC607;
RA Minakhin L.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RC607;
RX MEDLINE=89123092; PubMed=2536669;
RA Wang Y., Moore M., Levinson H.S., Silver S., Walsh C.T., Mahler I.;
RT "Nucleotide sequence of a chromosomal mercury resistance determinant
RT from a *Bacillus* sp. with broad-spectrum mercury resistance.";
RL J. Bacteriol. 171:83-92(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RC607;
RX MEDLINE=20026822; PubMed=10559175;
RA Gupta A., Phung L.T., Chakravarty L., Silver S.;
RT "Mercury resistance in *Bacillus cereus* RC607: transcriptional
RT organization and two new open reading frames.";
RL J. Bacteriol. 181:7080-7086(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RC607;
RA Endo G., Silver S., Huang C., Narita M.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08065; CAA69304.1; -; Genomic DNA.
DR EMBL; AB066362; BAB62437.1; -; Genomic DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006333; P:DNA transposition; IEA.
DR InterPro; IPR002513; Transposase_7.
DR Pfam; PF01526; Transposase_7; 1.
FT NON TER 1
FT SEQUENCE 54 AA; 6229 MW; 8939739E0F0D4803 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 15 REDL 18

RESULT 47
Q5QLQ2_ORYSA PRELIMINARY; PRT; 55 AA.
AC Q5QLQ2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein OSJNB0063G05.16.
GN Name=OSJNB0063G05.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijiishi S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi I., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohca I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003760; BAD73646.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 55 AA; 6600 MW; C1E151A6B294F958 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 15 REDL 18

RESULT 48
Q8F9J9_LEPIN PRELIMINARY; PRT; 55 AA.
AC Q8F9J9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LA0196;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of *Leptospira*
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011209; AAN47395.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6864 MW; 9D252ABA799938DA CRC64;

Query Match 100.0%; Score 20; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 4 REDL 7

RESULT 49
Q5E042_VIBF1 PRELIMINARY; PRT; 56 AA.
AC Q5E042;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=VFA0534;
OS *Vibrio fischeri* (strain ATCC 700601 / ES114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.

```

OX  NCBI_TaxID=312309;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX  PubMed=15703294; DOI=10.1073/pnas.0409900102;
RA  Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,
RA  Lestrich P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
RA  Stevens A., Visick K., Whistler C., Greenberg E.P.;
RT  "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
RT  with pathogenic congeners.";
RL  Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
DR  EMBL; CP000021; AAW87604.1; -; Genomic_DNA.
DR  InterPro; IPR010093; Xis.
DR  TIGRFAMs; TIGR01764; excise; 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 56 AA; 6520 MW; 6D58134FB659D9DA CRC64;

Query Match      100.0%; Score 20; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 REDL 4
Db  44 REDL 47

RESULT 50
Q4HAV9_9DEIO
ID  Q4HAV9_9DEIO PRELIMINARY; PRT; 57 AA.
AC  Q4HAV9;
DT  13-SEP-2005 (TrEMBLrel. 31, Created)
DT  13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT  13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE  Hypothetical protein.
DE  ORENAMES=DgeODRAFT_1362;
OS  Deinococcus geothermalis DSM 11300.
OC  Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC  Deinococcaceae; Deinococcus.
OX  NCBI_TaxID=319795;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=DSM 11300;
RG  US DOE Joint Genome Institute (JGI-PGF);
RA  Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA  Hammon N., Israni S., Pittluck S., Richardson P.;
RT  "Sequencing of the draft genome assembly of Deinococcus geothermalis
RT  DSM 11300.";
RL  Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=DSM 11300;
RG  US DOE Joint Genome Institute (JGI-ORNL);
RA  Larimer F., Land M.;
RT  "Annotation of the draft genome assembly of Deinococcus geothermalis
RT  DSM 11300.";
RL  Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; AAHE01000003; EAL83256.1; -; Genomic_DNA.
KW  Hypothetical protein.
SQ  SEQUENCE 57 AA; 6328 MW; A47FA5372B973436 CRC64;

Query Match      100.0%; Score 20; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 REDL 4
Db  15 REDL 18

Search completed: March 20, 2006, 07:57:28
Job time : 154.5 secs

```


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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:36 ; Search time 75.5 Seconds
(without alignments)
23.278 Million cell updates/sec

Title: US-09-673-707-9

Perfect score: 20

Sequence: 1 KDEL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	2	AAR41971 Mammalian
2	20	100.0	4	2	AAR48246 Endoplasm
3	20	100.0	4	2	AAR49442 Immunomod
4	20	100.0	4	2	AAR49584 Sequence
5	20	100.0	4	2	AAR95063 Mammalian
6	20	100.0	4	2	AAR94944 Microsoma
7	20	100.0	4	2	AAR95219 Pseudomon
8	20	100.0	4	2	AAR21969 Linker #3
9	20	100.0	4	2	AAW31861 Endoplasm
10	20	100.0	4	2	AAW56513 Endoplasm
11	20	100.0	4	2	AAW76396 Endoplasm
12	20	100.0	4	2	AAW52264 C-termina
13	20	100.0	4	2	AAW64614 Endomembr
14	20	100.0	4	2	AAW51437 C-termina
15	20	100.0	4	2	AAW61591 Endomembr
16	20	100.0	4	2	AAW51434 C-termina
17	20	100.0	4	2	ABB76201 Peptide u
18	20	100.0	4	2	AAW92911 Pseudomon
19	20	100.0	4	2	AAW85767 Endomembr
20	20	100.0	4	2	AAW30052 Organelle
21	20	100.0	4	2	AAW27177 Organelle
22	20	100.0	4	2	AAW49700 Pseudomon
23	20	100.0	4	2	AAW96345 Endoplasm
24	20	100.0	4	2	AAW92925 Pseudomon

25	20	100.0	4	2	AAV29637 KDEL pept
26	20	100.0	4	2	AAV25688 Membrane
27	20	100.0	4	3	AAV98152 Protein 1
28	20	100.0	4	3	AAO0912 Targeting
29	20	100.0	4	3	AAV70697 Rat endop
30	20	100.0	4	3	AAV56883 Endoplasm
31	20	100.0	4	3	AAV32395 Endoplasm
32	20	100.0	4	3	AAO03195 Endoplasm
33	20	100.0	4	3	AAV90442 Mammalian
34	20	100.0	4	3	AAV69694 Mammalian
35	20	100.0	4	3	AAV92046 Endoplasm
36	20	100.0	4	3	AAV93738 Amino aci
37	20	100.0	4	3	AAO30285 CD4+ T-ce
38	20	100.0	4	4	AAO35117 Adenoviru
39	20	100.0	4	4	AAO67291 Amino aci
40	20	100.0	4	4	AAO78315 ER lumen
41	20	100.0	4	4	AAO45947 Transdomi
42	20	100.0	4	4	AAO96038 Endoplasm
43	20	100.0	4	4	AAO70755 Endoplasm
44	20	100.0	4	4	AAO20214 Endoplasm
45	20	100.0	4	4	AAO31370 Amino aci
46	20	100.0	4	4	AAO03564 Peptide r
47	20	100.0	4	4	AAO84355 Amino aci
48	20	100.0	4	4	AAO48315 Endoplasm
49	20	100.0	4	4	AAO50814 Human end
50	20	100.0	4	4	AAO5817 Protein 1
51	20	100.0	4	4	AAO07199 Human ICA
52	20	100.0	4	4	AAO98995 C-termina
53	20	100.0	4	4	AAO82330 Endoplasm
54	20	100.0	4	4	AAO68569 Endoplasm
55	20	100.0	4	4	AAO76352 Synthetic
56	20	100.0	4	5	AAO20413 KDEL, ER
57	20	100.0	4	5	AAO51010 Leader pe
58	20	100.0	4	5	AAO07544 Amino aci
59	20	100.0	4	5	AAO99125 KDEL memb
60	20	100.0	4	5	AAO22202 Peptide r
61	20	100.0	4	5	AAO18835 Human cal
62	20	100.0	4	5	AAO14396 Endoplasm
63	20	100.0	4	5	AAO13432 Human KDE
64	20	100.0	4	5	AAO76185 Calreticu
65	20	100.0	4	5	AAO6731 Human XAG
66	20	100.0	4	5	ABG68877 Endoplasm
67	20	100.0	4	5	AAE28525 Endoplasm
68	20	100.0	4	5	AAE19017 Peptide #
69	20	100.0	4	5	AAE28690 Human cal
70	20	100.0	4	5	AAE94836 Endomembr
71	20	100.0	4	5	ABO09909 Radiolabe
72	20	100.0	4	5	ABG92970 Calreticu
73	20	100.0	4	5	AAE13263 KDEL pept
74	20	100.0	4	5	AAE17969 ER-retent
75	20	100.0	4	5	ABO75930 Endoplasm
76	20	100.0	4	5	ABO08104 Endoplasm
77	20	100.0	4	5	ADG68265 Polyimmun
78	20	100.0	4	5	ADG68265 Aspergill
79	20	100.0	4	5	ADG68265 Aspergill
80	20	100.0	4	5	ADG68265 Aspergill
81	20	100.0	4	5	ADG68265 Aspergill
82	20	100.0	4	6	ABU64905 Human cal
83	20	100.0	4	6	AAE33358 Endoplasm
84	20	100.0	4	6	ABU08976 Rat endop
85	20	100.0	4	6	AAO16771 Cytoplasm
86	20	100.0	4	6	AAE35569 ER-retent
87	20	100.0	4	6	AAE14821 Endoplasm
88	20	100.0	4	6	ABJ19274 Anti-huma
89	20	100.0	4	6	ABU64800 Human cal
90	20	100.0	4	6	ABP56565 Calreticu
91	20	100.0	4	6	ABP56575 Signal pe
92	20	100.0	4	6	ABP56611 Calreticu
93	20	100.0	4	6	ABR39556 Calreticu
94	20	100.0	4	6	ABU09487 Endoplasm
95	20	100.0	4	6	ABR39588 Amino aci
96	20	100.0	4	6	ABR39418 Endoplasm
97	20	100.0	4	6	ABU14033 Calreticu

98	20	100.0	4	6	ABP71099	Peptide 1
99	20	100.0	4	6	Aae36304	Endoplasm
100	20	100.0	4	6	Abp72886	Human cal
101	20	100.0	4	6	Abu09657	Calreticu
102	20	100.0	4	6	Aae32718	Calreticu
103	20	100.0	4	6	Abg72269	Peptide u
104	20	100.0	4	6	Aae34842	Endoplasm
105	20	100.0	4	6	Abu96669	ER retent
106	20	100.0	4	6	Aae37781	Localisat
107	20	100.0	4	6	Aao31116	Endoplasm
108	20	100.0	4	6	Aao32272	ER recent
109	20	100.0	4	6	Ada50227	KDEL pept
110	20	100.0	4	6	Abri61855	Pseudomon
111	20	100.0	4	6	Abu63380	Rat ER re
112	20	100.0	4	6	Ada26346	Canine GR
113	20	100.0	4	6	Abc32836	Cytoplasm
114	20	100.0	4	7	Ada07010	Calreticu
115	20	100.0	4	7	Ada08301	Calreticu
116	20	100.0	4	7	Adb66860	Fusion nu
117	20	100.0	4	7	Ada44808	Endoplasm
118	20	100.0	4	7	Adc34608	Mammalian
119	20	100.0	4	7	Aae38954	Calreticu
120	20	100.0	4	7	Adc26554	Golgi ret
121	20	100.0	4	7	Aae39838	Human end
122	20	100.0	4	7	Adc84560	Carboxyl
123	20	100.0	4	7	Adc28914	Calreticu
124	20	100.0	4	7	Adel0750	Structura
125	20	100.0	4	7	Adf39276	KDEL loca
126	20	100.0	4	7	Adf32312	Calreticu
127	20	100.0	4	7	Adf28981	ER reteti
128	20	100.0	4	7	Adf57572	Rat endop
129	20	100.0	4	7	Adf90408	Calreticu
130	20	100.0	4	7	Adh92032	Cytoplasm
131	20	100.0	4	7	Adj53825	Calreticu
132	20	100.0	4	8	Adf93265	Plant alb
133	20	100.0	4	8	Adg25840	Pseudomon
134	20	100.0	4	8	Adf94964	Endoplasm
135	20	100.0	4	8	Adh11621	Human KDE
136	20	100.0	4	8	Adh61900	Human tar
137	20	100.0	4	8	Adh51589	Human pep
138	20	100.0	4	8	Adi36229	Human cal
139	20	100.0	4	8	Adk15769	ER-retain
140	20	100.0	4	8	Adm13763	Fusion pr
141	20	100.0	4	8	Adm35872	Endoplasm
142	20	100.0	4	8	Adl23799	Calreticu
143	20	100.0	4	8	Adm68937	Endoplasm
144	20	100.0	4	8	Adl91589	Endoplasm
145	20	100.0	4	8	Adl14837	Yeast end
146	20	100.0	4	8	Adn49849	C-termina
147	20	100.0	4	8	Adn07009	Pseudomon
148	20	100.0	4	8	Adn07009	Pseudomon
149	20	100.0	4	8	Adn49386	Delta 6-d
150	20	100.0	4	8	Adn37764	Endoplasm

RESULT 1

AAR41971 standard; peptide; 4 AA.

XX AAR41971;

AC AAR41971;

XX

XX

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 22-OCT-1993 (first entry)

XX

DE Mammalian endoplasmic reticulum retention signal.

XX

XX yeast expression cassette; yeast alpha-factor leader; KEX2p;

KW heterologous protein production; mating pheromone; YAP3;

KW dibasic processing endoprotease.

XX Abp71099

OS Aae36304

XX Endoplasm

PN Abp72886

XX Human cal

XX Abu09657

XX Calreticu

XX Aae32718

XX Calreticu

XX Abg72269

XX Peptide u

XX Aae34842

XX Endoplasm

XX Abu96669

XX ER retent

XX Aae37781

XX Localisat

XX Aao31116

XX Endoplasm

XX Aao32272

XX ER recent

XX Ada50227

XX KDEL pept

XX Abri61855

XX Pseudomon

XX Abu63380

XX Rat ER re

XX Ada26346

XX Canine GR

XX Abc32836

XX Cytoplasm

XX Ada07010

XX Calreticu

XX Ada08301

XX Calreticu

XX Adb66860

XX Fusion nu

XX Ada44808

XX Endoplasm

XX Adc34608

XX Mammalian

XX Aae38954

XX Calreticu

XX Adc26554

XX Golgi ret

XX Aae39838

XX Human end

XX Adc84560

XX Carboxyl

XX Adc28914

XX Calreticu

XX Adel0750

XX Structura

XX Adf39276

XX KDEL loca

XX Adf32312

XX Calreticu

XX Adf28981

XX ER reteti

XX Adf57572

XX Rat endop

XX Adf90408

XX Calreticu

XX Adh92032

XX Cytoplasm

XX Adj53825

XX Calreticu

XX Adf93265

XX Plant alb

XX Adg25840

XX Pseudomon

XX Adf94964

XX Endoplasm

XX Adh11621

XX Human KDE

XX Adh61900

XX Human tar

XX Adh51589

XX Human pep

XX Adi36229

XX Human cal

XX Adk15769

XX ER-retain

XX Adm13763

XX Fusion pr

XX Adm35872

XX Endoplasm

XX Adl23799

XX Calreticu

XX Adm68937

XX Endoplasm

XX Adl91589

XX Endoplasm

XX Adl14837

XX Yeast end

XX Adn49849

XX C-termina

XX Adn07009

XX Pseudomon

XX Adn49386

XX Delta 6-d

XX Adn37764

XX Endoplasm

ALIGNMENTS

RESULT 1

AAR41971

XX AAR41971 standard; peptide; 4 AA.

XX

AC AAR41971;

XX

XX

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 22-OCT-1993 (first entry)

XX

DE Mammalian endoplasmic reticulum retention signal.

XX

XX yeast expression cassette; yeast alpha-factor leader; KEX2p;

KW heterologous protein production; mating pheromone; YAP3;

KW dibasic processing endoprotease.

XX Mammalia.

OS EP548012-A1.

XX

PN

XX

XX 23-JUN-1993.

XX

XX

XX 08-DEC-1992; 92EP-00810964.

XX

XX 16-DEC-1991; 91EP-00810984.

XX

XX (CIBA) CIBA GEIGY AG.

XX (NOVS) NOVARTIS AG.

XX Chaudhuri B, Stephan C, Seeboth P, Riezman H;

XX WPI; 1993-198976/25.

XX Endoplasmic reticulum-located recombinant di:basic endoprotease - used in

XX host cells to raise ratio of active, correctly folded heterologous

XX protein.

XX Disclosure; Page 3; 30pp; English.

XX

XX Dibasic endoproteases of the invention are localised to the endoplasmic

XX reticulum of yeast host cells via ER-retention signals. A preferred

XX retention signal is the tetrapeptide KDEL functional in mammalian cells.

XX See also AA042671, AA042672 and AAR41971-2. (Updated on 10-MAR-2003 to

XX add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)

XX (Updated on 25-MAR-2003 to correct PA field.)

XX

XX Sequence 4 AA;

XX

Query Match 100.0%; Score 20; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

DB 1 KDEL 4

RESULT 2

AAR48246

XX AAR48246 standard; peptide; 4 AA.

XX

XX AAR48246;

AC

XX

XX 25-MAR-2003 (revised)

DT 29-JUL-1994 (first entry)

XX

XX Endoplasmic reticulum retention signal KDEL.

XX

XX Single chain antibody; sFv; heavy chain; light chain; kappa;

XX variable domain; hydrophilic linker; antibodies;

XX endoplasmic reticulum retention.

XX

XX Synthetic.

XX

XX WO9402610-A1.

XX

XX

XX 03-FEB-1994.

XX

XX

XX 16-JUL-1993; 93WO-US006735.

XX

XX

XX 17-JUL-1992; 92US-00916939.

XX

XX 17-MAR-1993; 93US-00045274.

XX

XX (DAND) DANA FARBER CANCER INST INC.

XX

XX Marasco WA, Haseltine WA;

XX

XX WPI; 1994-048868/06.

XX Intracellular binding of antigens - by using antibody targetting with
 PT vector system, for e.g. tumour suppression.
 XX
 PS Claim 32; Page 99; 155pp; English.
 XX
 CC New vector systems comprise a sequence adapted for intracellular delivery
 CC and expression contg. a promoter operably linked to an antibody gene
 CC encoding an antibody which binds to a specific target antigen. The
 CC antibody is esp. a single chain antibody in which the heavy and light
 CC chain variable regions are joined via a hydrophilic linker peptide.
 CC Localisation sequences are pref. included in the constructs. See AAR48246
 CC -9 and AAR48252-3 for pref. (known) endoplasmic reticulum retention
 CC signals. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 3

AAR49442
 ID AAR49442 standard; protein; 4 AA.

XX AC AAR49442;

XX 25-MAR-2003 (revised)
 DT 16-SEP-1994 (first entry)

XX Immunomodulatory trafficking sequence #1.

XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;
 KW major histocompatibility complex; class II; allotype; type I diabetes;
 KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
 KW multiple sclerosis; transplant rejection; vaccine; MHC.

XX Homo sapiens.

XX WO9404171-A1.

XX 03-MAR-1994.

XX 11-AUG-1993; 93WO-US007545.

XX 11-AUG-1992; 92US-00925460.

PR 15-JUN-1993; 93US-00077255.

XX (HARD) HARVARD COLLEGE.

XX Urban RG, Chiciz RM, Vignali DA, Hedley ML, Stern LJ;
 PI Strominger JL;

XX WPI; 1994-082825/10.

XX Novel immunomodulatory peptide(s) and nucleic acids - useful for
 PT treatment of auto-immune diseases, transplant rejection and for
 PT vaccination.

XX Claim 13; Page 94; 139pp; English.

XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
 CC fragments of naturally-occurring immunomodulatory proteins. These
 CC fragments are between 10-30 residues in length and bind to a human major
 CC histocompatibility complex (MHC) class II allotype. These peptides may be
 CC used for therapy of autoimmune diseases, such as type I diabetes,
 CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant
 CC rejection. They may also be used for vaccination providing an exclusively

CC T-cell-mediated response, which can be class I or class-II based, or
 CC both, depending on the length and character of the immunogenic peptides.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 4

AAR49584
 ID AAR49584 standard; peptide; 4 AA.

XX AC AAR49584;

XX 25-MAR-2003 (revised)
 DT 15-SEP-1994 (first entry)

XX Sequence of endoplasmic reticulum (ER) retention peptide.

XX Endoplasmic reticulum; ER; trafficking sequence.

XX Synthetic.

XX WO9404557-A1.

XX 03-MAR-1994.

XX 11-AUG-1992; 92WO-US006692.

XX 11-AUG-1992; 92WO-US006692.

XX (HARD) HARVARD COLLEGE.

XX Urban RG, Chiciz RM, Vignali DAA, Hedley ML, Stern LJ;
 PI Strominger JL;

XX WPI; 1994-083102/10.

XX New peptide binding to MHC class II allotype - useful for treating auto-
 PT immune diseases, transplant rejection and for immunisation.

XX Claim 20; Page 49; 60pp; English.

XX A trafficking sequence is an AA sequence which functions to control
 CC intracellular trafficking (directed movement from organelle to organelle
 CC or to the cell surface) of a polypeptide to which it is attached. Such
 CC trafficking sequences might traffic the polypeptide to ER, a lysosome, or
 CC an endosome, and include signal peptides, ER retention peptides such as
 CC AAR49584; and lysosome-targeting peptides such as AAR49585 and AAR49586.
 CC An example of a signal peptide with such a function is the signal peptide
 CC of MHC class II alpha (AAR49587). (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 5

AAR95063
ID AAR95063 standard; peptide; 4 AA.
XX
AC AAR95063;
XX
DT 22-AUG-1996 (first entry)
XX
DE Mammalian endoplasmic reticulum retention signal.
XX
KW Nucleic acid transfer system; gene transfer; gene therapy;
KW cell targeting; multidomain protein; vector; cancer;
KW endoplasmic reticulum.
XX
OS Synthetic.
XX
FN WO9613599-A1.
XX
PD 09-MAY-1996.
XX
PF 31-OCT-1995; 95WO-EP004270.
XX
PR 01-NOV-1994; 94EP-00810627.
XX
PA (WELS/) WELS W.
XX
PI Wels W, Fominaya J;
XX
XX WPI; 1996-239505/24.
XX
XX Nucleic acid transfer system for gene therapy, e.g. against cancer -
PT includes toxin translocation domain to target nucleic acid to specific
PT cell.
XX
PS Disclosure; Page 11; 106pp; English.
XX
CC Endoplasmic reticulum retention signals include a mammalian signal
CC (AAR95063), a bacterial signal (AAT05064) from Pseudomonas exotoxin, and
CC a yeast signal (AAR95065). The signal may form part of a multidomain
CC protein (see also AAR95053-58) that is used with an effector nucleic acid
CC for the transfer of nucleic acids to targeted cells as a means of gene
CC therapy. The endoplasmic reticulum retention signal functions to affect
CC intracellular routing of the internalized protein/nucleic acid complex
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db ||||
1 KDEL 4

RESULT 6
AAR94944
ID AAR94944 standard; protein; 4 AA.
XX
AC AAR94944;
XX
DT 31-OCT-1996 (first entry)
XX
DE Microsomal retention signal.
XX
KW Toxin; subunit; vaccine; transgenic plant; immunogen; antigen; adjuvant;
KW immunisation.
XX
OS Synthetic.
XX
FN WO9612801-A1.
XX
PD 02-MAY-1996.
XX

PF 24-OCT-1995; 95WO-US013376.
XX
PR 24-OCT-1994; 94US-00328716.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
PA (TULA) TULANE EDUCATIONAL FUND.
XX
PI Arntzen CJ, Mason HS, Haq TA, Clements JD;
XX
XX WPI; 1996-230602/23.
XX
XX Transgenic plants contg. E. coli heat labile enterotoxin subunits - used
PT as oral vaccines for animals which consume the plant.
XX
XX Example 13; Page 95; 130pp; English.
XX
CC A transgenic plant comprising or expressing a DNA sequence encoding an
CC immunogenic agent can be used as an oral vaccine for animals. The
CC vaccine is administered by the oral consumption of the plant and provides
CC the first known functional method for immunising animals using transgenic
CC plants, where the plants express bacterial antigens that act as both
CC immunogens and adjuvants. The method provides an inexpensive production
CC and delivery system for such antigens to animals. This sequence acts as a
CC microsomal retention signal and was used to modify the LT-B Escherichia
CC coli toxin subunit C-terminal sequence. The sequence coding for the whole
CC LT-B gene was used in the construction of such a transgenic plant. The
CC immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B
CC subunit) or optionally LT-A or CT-A
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db ||||
1 KDEL 4

RESULT 7
AAR95219
ID AAR95219 standard; protein; 4 AA.
XX
AC AAR95219;
XX
DT 16-DEC-1996 (first entry)
XX
DE Pseudomonas exotoxin modified C-terminal sequence.
XX
KW Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
KW detection; imaging; immunotoxin; targeting; assay; immunoassay;
KW Lewis(Y) carbohydrate antigen.
XX
OS Pseudomonas sp.
XX
FN WO9613594-A1.
XX
PD 09-MAY-1996.
XX
PF 26-OCT-1995; 95WO-US013811.
XX
PR 28-OCT-1994; 94US-00331396.
PR 28-OCT-1994; 94US-00331397.
PR 28-OCT-1994; 94US-00331398.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;
PI Fitzgerald D, Brinkmann U, Pai L;
XX
XX WPI; 1996-251462/25.
XX

PT Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.
 PS Disclosure; Page 14; 116pp; English.
 XX
 CC A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and heavy
 CC chains of an antibody (Ab) fused together, and an effector molecule,
 CC where the fusion protein or Ab has the binding specificity of monoclonal
 CC Ab (MAb) B1, B3 or B5, can be used for the production of such fusion
 CC proteins or antibodies. The fusion proteins can be used in compositions
 CC as an immunotoxin to inhibit tumour cell growth. The single chain
 CC antibody can be used to detect the presence or absence of cells bearing a
 CC Lewis(X) carbohydrate antigen in a patient. The antibodies are also
 CC useful as multiple targeting moieties, providing at least 2 kinds of
 CC biological activity. They can also be used in diagnostic assays and for
 CC the imaging of tumours when attached to a radiolabel and for the
 CC pathological diagnosis of tumours. Humanised antibodies are less
 CC immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable
 CC for long term treatment. The effector molecule used is preferably a drug
 CC or cytotoxin which then produces an immunotoxin capable of selectively
 CC killing particular cells. Preferred toxins are the Pseudomonas exotoxin
 CC or Diphtheria toxin. These are both highly toxic compounds and so are
 CC modified to eliminate domain Ia of the Pseudomonas toxin, various amino
 CC acid deletions in domains II and III, single amino acid substitutions and
 CC addition of one or more sequences at the C-terminal end. The wild type C-
 CC terminal sequence of the Pseudomonas exotoxin is given in AAR95221
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEL 4
 Db | | | |
 1 KDEL 4
 RESULT 8
 AAW21969
 ID AAW21969 standard; peptide; 4 AA.
 AC
 AC AAW21969;
 XX
 DT 03-DEC-1997 (first entry)
 XX
 DE Linker #3 for immunotoxin containing Pseudomonas exotoxin.
 XX
 KW PCR; primer; amplify; polymerase chain reaction; antibody; immunotoxin;
 KW variable heavy chain; VH; murine monoclonal antibody; Lewisy; carcinoma;
 KW carbohydrate antigen; Pseudomonas exotoxin; proteolytic activation;
 KW cytotoxic activity; tumour; autoimmune condition; rheumatoid arthritis;
 KW graft versus host disease; organ transplant rejection; type I diabetes;
 KW multiple sclerosis; systemic lupus erythematosus; myasthenia gravis;
 KW T cell; B cell; cytosol; bone marrow; transplant; therapy.
 XX
 OS Synthetic.
 XX
 XX WO9713529-A1.
 XX
 XX 17-APR-1997.
 XX
 XX 11-OCT-1996; 96WO-US016327.
 XX
 XX 13-OCT-1995; 95US-0005388P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Pastan I, Kuan C;
 XX
 XX WPI; 1997-235666/21.
 XX

PT Immuno:toxin(s) comprising Pseudomonas exotoxin linked to di:sulphide
 PT stabilised variable heavy and light chain regions of an antibody - useful
 PT for killing target cells bearing characteristic marker.
 XX
 PS Claim 9; Page 50; 64pp; English.
 XX
 CC AAW21967-W21969 represent linkers used in the immunotoxins of the
 CC invention. The immunotoxins bind to target cells, and comprise, a
 CC Pseudomonas exotoxin (PE) that does not need proteolytic activation for
 CC cytotoxic activity fused to a VH framework region of an Fv antibody (Ab)
 CC fragment. The VH chain region is bound through at least one disulphide
 CC bond to a variable light (VL) chain framework region. The PE is lacking
 CC residues 1-279 and is at least 10-fold more cytotoxic to the target cells
 CC than an immunotoxin comprising PE attached to a VH chain framework region
 CC of an Fv Ab fragment lacking a disulphide bond to a VL chain framework
 CC region. These sequences are used to join the VH chain region to the PE.
 CC The immunotoxins can be used for killing target cells in the treatment of
 CC tumours, autoimmune conditions, graft versus host disease, organ
 CC transplant rejection, type I diabetes, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, myasthenia gravis, etc, all
 CC caused by T and B cells. They can also be used to deliver an antibody to
 CC the cytosol of a cell, and in vitro in the elimination of harmful cells
 CC from bone marrow before transplant. The immunotoxins have high
 CC cytotoxicity to target cells and a small size to provide greater
 CC penetration to target cells
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEL 4
 Db | | | |
 1 KDEL 4
 RESULT 9
 AAW31861
 ID AAW31861 standard; peptide; 4 AA.
 XX
 AC AAW31861;
 XX
 DT 06-MAY-1998 (first entry)
 XX
 DE Endoplasmic reticulum retention peptide.
 XX
 KW RNA-loaded antigen presenting cell; trafficking sequence; APC production;
 KW tumour formation; pathogen infection; antigenic epitope; immune response;
 KW T cell proliferation; cytotoxic T lymphocyte; adoptive immunotherapy;
 KW therapy; TAE; CTL; PAE; endoplasmic reticulum retention peptide.
 XX
 OS Synthetic.
 XX
 XX WO9741210-A1.
 XX
 XX 06-NOV-1997.
 XX
 XX 30-APR-1997; 97WO-US007317.
 XX
 XX 30-APR-1996; 96US-00640444.
 XX
 XX (UYDU-) UNIV DUKE.
 XX
 XX Nair SK, Boczkowski DJ, Gilboa E;
 XX
 XX WPI; 1997-549715/50.
 XX
 PT Use of RNA-loaded antigen presenting cells - to induce T-cell
 PT proliferation for the treatment or prevention of tumour formation or
 PT pathogen infection.
 XX
 PS Claim 49; Page 38; 47pp; English.

XX This sequence represents a endoplasmic reticulum retention peptide, and
 CC can be used in the method of the invention. The method is for producing
 CC an RNA-loaded antigen presenting cell (APC) that presents on its surface
 CC a tumour or pathogen antigenic epitope (TAE or PAE respectively) that
 CC induces T cell proliferation and an immune response against the tumour or
 CC pathogen, and comprises introducing into an APC in vitro, RNA that
 CC encodes the antigen. The RNA-loaded APCs can be used to stimulate
 CC cytotoxic T lymphocyte (CTL) proliferation ex vivo or in vivo. The ex
 CC vivo expanded CTL can be administered to a patient in a method of
 CC adoptive immunotherapy. The methods can be used for treating or
 CC preventing tumour formation or pathogen infection caused by e.g. HIV,
 CC hepatitis, influenza, poliomyelitis, measles, herpes, mumps or rubella
 CC viruses, Salmonella, Shigella or Enterobacter. The method circumvents the
 CC need to purify RNA or isolate and identify a TAE or PAE
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 ||||
 DB 1 KDEL 4

RESULT 10
 AAW56513
 ID AAW56513 standard; peptide; 4 AA.

AC AAW56513;

XX 28-SEP-1998 (first entry)

XX Endoplasmic reticulum recycling peptide.

XX Intracellular targeting sequence; endoplasmic reticulum; DNA vaccine;
 KW Genetic immunisation; allergy; autoimmune disease; cancer; infection;
 KW psoriasis.

XX Synthetic.

XX WO9817323-A1.

XX 30-APR-1998.

XX 23-OCT-1997; 97WO-US019545.

XX 23-OCT-1996; 96US-0029592P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Williams WV, Madaio M, Weiner DB;

XX WPI; 1998-261198/23.

XX Plasmid encoding immunogenic target protein - used in, e.g. protective or
 PT therapeutic vaccines against allergy, cancer, microbial infection or auto
 PT -immune disease.

XX Claim 7; Page 62; 84pp; English.

XX This peptide, when joined to the C-terminus of a protein, acts as an
 CC endoplasmic reticulum (ER) recycling signal that localises the protein
 CC from the Golgi body back to the ER when expressed in a cell. A claimed
 CC novel plasmid comprises a sequence, linked to regulatory elements, that
 CC encodes an immunogenic target protein that includes, or is linked to, an
 CC intracellular targeting sequence (ITS) such as this peptide. Other ITS
 CC peptides (see AAW56512 and AAW56514) are provided that direct
 CC localisation in the lysosome or the ER. The novel plasmid is used as a
 CC protective or therapeutic DNA vaccine to immunise against the immunogenic
 CC target protein (claimed), particularly in cases of allergy, cancer (or

CC other proliferative diseases such as psoriasis), microbial infection or
 CC autoimmune disease, e.g. rheumatoid arthritis, insulin-dependent diabetes
 CC mellitus, Crohn's disease, asthma, pernicious anaemia and many others. A
 CC particular use is against pathogens that, at least for part of their life
 CC cycle, are intracellular, e.g. hepatitis C, HIV, Neisseria gonorrhoeae,
 CC Listeria and Shigella. The cytotoxic T cell response is enhanced by
 CC delivering the immunogenic target protein to the ER
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 ||||
 DB 1 KDEL 4

RESULT 11
 AAW76396
 ID AAW76396 standard; peptide; 4 AA.

XX AAW76396;

XX 11-JAN-1999 (first entry)

XX Endoplasmic reticulum transport signal consensus.

XX Exotoxin A; ETA; drug delivery; membrane transport;
 KW endoplasmic reticulum.

XX Synthetic.

XX WO9842876-A1.

XX 01-OCT-1998.

XX 24-MAR-1998; 98WO-US005710.

XX 26-MAR-1997; 97US-0042056P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Draper RK;

XX WPI; 1998-532023/45.

XX Delivering compounds to cells as new conjugate with detoxified exotoxin A
 PT - able to cross membranes and deliver to the cytoplasm, e.g. nucleic
 PT acids, antibodies, tumour suppressors etc.

XX Disclosure; Page 8; 76pp; English.

XX This peptide is the consensus intracellular transport signal used for
 CC returning back to the endoplasmic reticulum (ER) proteins that have the
 CC escaped the ER and entered to Golgi complex. The mechanism involves the
 CC KDEL receptor. The KDEL motif can replace a REDL motif (see AAW76395)
 CC present at the C-terminal end of Pseudomonas aeruginosa exotoxin A (ETA,
 CC see AAW76391). This motif is important in the intracellular transport and
 CC cytotoxicity of ETA. This suggests that ETA interacts with the KDEL
 CC receptor and that ETA may reach the interior of the ER before penetrating
 CC the cytosol. The invention provides a means of delivering compounds to
 CC cells as conjugates with modified ETA. The modified ETA is able to cross
 CC membranes and deliver e.g. therapeutic agents to the cytoplasm, such as
 CC nucleic acids, peptides, peptide nucleic acids, single chain antibodies
 CC and tumour suppressors

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 12
 AAW52264
 ID AAW52264 standard; peptide; 4 AA.
 XX AC AAW52264;
 XX DT 18-JUN-1998 (first entry)
 XX DE C-terminal fragment of pseudomonas exotoxin.
 XX KW Pseudomonas exotoxin; PE; cytotoxic.
 XX OS Pseudomonas sp.
 XX PN US5705163-A.
 XX PD 06-JAN-1998.
 XX PF 05-JUN-1995; 95US-00461233.
 XX PR 02-JAN-1990; 90US-00459635.
 XX PR 12-MAY-1990; 90US-00522563.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Fitzgerald D, Pastan I, Chaudhary VK;
 XX DR WPI; 1998-086092/08.
 XX PT Methods for killing target cells - with recombinant Pseudomonas exotoxin fusion proteins.
 XX PS Claim 8; Col 14; 12pp; English.
 XX CC This sequence represents a C-terminal fragment of a Pseudomonas exotoxin (PE). This sequence can be used in the method of the invention for killing a target cell, which comprises contacting the cell with a recombinant Pseudomonas exotoxin (PE) having: (a) a recognition molecule that binds to the target cell and is inserted in domain III after amino acid 600 and before amino acid 613 of the PE, and (b) a carboxy-terminal sequence of 4-16 amino acids that permits translocation of the PE into the cytosol of the target cell. The insertion of a recognition molecule allows selective killing of target cells without significant cytotoxicity to other cells not recognised

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 13
 AAW64614
 ID AAW64614 standard; protein; 4 AA.
 XX AC AAW64614;
 XX DT 17-OCT-2003 (revised)
 XX DT 03-NOV-1998 (first entry)
 XX DE Endomembrane retention signal peptide.
 XX

KW Target; imaging agent; epithelium; transepithelial transport; diagnosis; transcytosis; disease; basolateral; internalisation; J chain.
 XX unidentified.
 XX OS
 XX PN WO9830591-A1.
 XX PD 16-JUL-1998.
 XX PF 09-JAN-1998; 98WO-US000339.
 XX PR 10-JAN-1997; 97US-00782480.
 XX PA (EPIC-) EPICYTE PHARM INC.
 XX PI Hiatt AC, Hein MB, Fitchen JH;
 XX DR WPI; 1998-399066/34.
 XX PT New epithelial tissue targeting agent - used to deliver imaging agents to an epithelial surface for internalisation; useful in diagnosis.
 XX PS Example 1c; Page 90; 118pp; English.
 XX CC This sequence represents an endomembrane retention signal which is used in a method involving the construction of a target molecule from human J chain protein fragments. This construct is used in a method to target imaging agents to epithelial surfaces at which they may remain or undergo transepithelial transport via transcytosis. At least one imaging agent is linked to the targeting molecule comprising a polypeptide that (a) forms a closed covalent loop, (b) contains at least 3, preferably 4, peptide domains having beta-sheet character separated by domains lacking beta-sheet character and (c) is not full length dimeric IgA. The imaging agents are useful in the diagnosis of disease. The target molecule is also capable of specifically binding to a basolateral factor associated with an epithelial surface to cause internalisation of a biological agent linked to the target molecule. (Updated on 17-OCT-2003 to standardise OS field)

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 14
 AAW51437
 ID AAW51437 standard; peptide; 4 AA.
 XX AC AAW51437;
 XX DT 02-SEP-1998 (first entry)
 XX DE C-terminal sequence of endoplasmic reticulum retained proteins.
 XX KW Endoplasmic reticulum; carboxy terminus; Golgi apparatus;
 XX KW glycosyltransferase; membrane anchor; oligosaccharide synthesis.
 XX OS Synthetic.
 XX PN US5776772-A.
 XX PD 07-JUL-1998.
 XX PF 30-JAN-1996; 96US-00593865.
 XX PR 24-OCT-1989; 89US-00426577.
 XX PR 27-MAY-1992; 92US-00849045.

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 1 KDEL 4

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 10-MAR-1994; 94US-00209604.
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Paulson JG, Colley KJ, Browne JK, Adler B, Weinstein J;
 PI Ujita-Lee E;
 PI
 XX WPI; 1998-398046/34.
 DR
 XX Expression cassette for producing glycosyltransferase in secretable form
 PT - lacking membrane anchor and Golgi retention signal, used for synthesis
 PT of oligosaccharide(s).
 XX
 XX Disclosure; Col 3; 16pp; English.
 PS
 XX The invention relates to expression cassettes which contain a promoter
 CC and a DNA sequence encoding a secreted glycosyltransferase that lacks the
 CC membrane anchor and the Golgi retention signal. The glycosyl-
 CC transferases are used in enzymatic oligosaccharide synthesis. They are
 CC produced in a soluble form that is secreted into the culture medium
 CC without loss of enzymatic activity, resulting in increased production and
 CC simpler recovery (free of any membrane-bound glycosyl- transferase),
 CC compared with extraction from mammalian tissue. The present sequence
 CC represents a carboxy-terminal sequence sufficient for retention of a
 CC protein in the endoplasmic reticulum
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEL 4
 DB ||||
 1 KDEL 4
 RESULT 15
 AAW61591
 ID AAW61591 standard; peptide; 4 AA.
 XX
 AC AAW61591;
 XX
 XX 27-OCT-1998 (first entry)
 DT
 XX Endomembrane retention signal.
 DE
 XX J chain; targeting molecule; epithelial; beta-sheet; asthma; cancer;
 KW inflammatory disorder; autoimmune disorder; celiac disease; colitis;
 KW pneumonia; cystic fibrosis.
 XX
 XX Synthetic.
 OS
 XX WO9830592-A1.
 PN
 XX 16-JUL-1998.
 PD
 XX 09-JAN-1998; 98WO-US000542.
 XX
 XX 10-JAN-1997; 97US-00782481.
 PR
 XX (EPIC-) EPICYTE PHARM INC.
 PA
 XX Hein MB, Hiatt AC, Fitchen JH;
 PI
 XX WPI; 1998-399067/34.
 DR
 XX New epithelial tissue targeting agent - used to deliver biologically
 PT active compounds to an epithelial surface for internalisation.
 PT
 XX Example 1; Page 48; 142pp; English.
 PS
 XX The endomembrane retention signal is used in the synthesis of a targeting

CC molecule (TM). The TMs are used to target biological agents to epithelial
 CC surfaces at which they can be internalised. The TMs comprise a
 CC polypeptide that: (a) forms a closed covalent loop; (b) contains at least
 CC 3, preferably 4, peptide domains having beta-sheet character separated by
 CC domains lacking beta-sheet character; and (c) is not full length dimeric
 CC IgA. The TMs are useful to prevent and/or treat diseases associated with
 CC epithelial surfaces, e.g. asthma, cancer, (myco)bacterial, viral or
 CC fungal infection, inflammatory disorders, autoimmune disorders, celiac
 CC disease, colitis, pneumonia and cystic fibrosis
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEL 4
 DB ||||
 1 KDEL 4
 RESULT 16
 AAW51434
 ID AAW51434 standard; peptide; 4 AA.
 XX
 AC AAW51434;
 XX
 XX 02-SEP-1998 (first entry)
 DT
 XX C-terminal sequence of localisation peptides for the ER.
 DE
 XX Bifunctional chelating polysaccharide; targeting peptide; heparin;
 KW nuclear localisation; fluorescent indicator; dextran; ficol; glycogen;
 KW amylopectin; mannan; inulin; starch; agarose; cellulose; ER;
 KW endoplasmic reticulum.
 XX
 XX Synthetic.
 OS
 XX US5773227-A.
 PN
 XX 30-JUN-1998.
 PD
 XX 23-JUN-1993; 93US-00082269.
 PF
 XX 23-JUN-1993; 93US-00082269.
 PR
 XX (MOLE-) MOLESCULAR PROBES INC.
 PA
 XX Meyer T, Kuhn MA, Allbritton NL;
 PI
 XX WPI; 1998-386995/33.
 DR
 XX Bifunctional chelating polysaccharides used for analysing intracellular
 PT ion levels - have chelating moieties attached which act as a fluorescent
 PT indicator in the presence of selected metal ions.
 XX
 XX Disclosure; Col 9; 29pp; English.
 PS
 XX The invention relates to a water soluble polysaccharide with a molecular
 CC weight greater than 1000 Daltons covalently attached to (a) at least one
 CC chelating moiety selective for a monovalent or divalent metal ion (to act
 CC as a fluorescent indicator for the metal ion) and (b) at least one
 CC targeting peptide (to localise the compound to the inside of a cellular
 CC organelle). Preferably the polysaccharide is dextran, ficol, heparin,
 CC glycogen, amylopectin, mannan, inulin, starch, agarose or cellulose with
 CC a molecular weight less than 3,000,000. The metal ion is preferably Na+,
 CC K+, Li+, Ca2+ or Mg2+. The compounds are useful for analysing intra-
 CC cellular ion levels, especially Ca2+. The present sequence represents a
 CC carboxyl terminal sequence commonly shared by localisation peptides for
 CC the endoplasmic reticulum (ER)
 XX
 XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 17

ABW76201
 ID ABB76201 standard; peptide; 4 AA.

XX
 AC ABB76201;

XX 05-AUG-2002 (first entry)

XX Peptide used to modify Pseudomonas exotoxin.

XX Exotoxin; Pseudomonas; immunotoxin; mesothelin; scFv; mesothelioma;
 KW ovarian cancer; stomach cancer; squamous cell cancer; antitumor;
 KW therapy; diagnosis.

XX Synthetic.

XX WO9928471-A2.

XX 10-JUN-1999.

XX 25-NOV-1998; 98WO-US025270.

XX 01-DEC-1997; 97US-0067175P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Pastan IH, Chowdhury PS;

XX WPI; 1999-371123/31.

XX New anti-mesothelin antibodies.

XX Disclosure; Page 29; 63pp; English.

XX The present sequence is a peptide that can be added to the C-terminal end
 CC of a Pseudomonas exotoxin (PE) to produce a modified PE. Claimed
 CC immunoconjugates comprise a therapeutic agent, such as PE or a cytotoxic
 CC fragment of PE, and an anti-mesothelin antibody, such as scFv SS (see
 CC ABB76197), and are obtained by recombinant methods. The recombinant
 CC immunoconjugates are used in a claimed method for inhibiting the growth
 CC of a malignant cell that expresses mesothelin on its cell surface,
 CC especially in mesothelioma, ovarian cancer, stomach cancer or squamous
 CC cell cancer

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 18

AAW92911
 ID AAW92911 standard; protein; 4 AA.

XX
 AC AAW92911;

XX 17-MAY-1999 (first entry)

XX Pseudomonas sp. exotoxin A PE ER retention peptide motif #3.

XX

KW Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;
 KW antibody production; non-native epitope; immune response; antigen;
 KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;
 KW secretory; IgA-mediated; mucosal surface; IgA antibody; retention domain;
 KW endoplasmic reticulum.

XX Pseudomonas sp.

XX WO9902712-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014336.

XX 11-JUL-1997; 97US-0056924P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX (GETH) GENENTECH INC.

XX Fitzgerald DJ, Mresny RJ;

XX WPI; 1999-120913/10.

XX New Pseudomonas exotoxin chimeric immunogens - comprise a foreign epitope
 PT for producing an immune response to pathogens, e.g. virus, bacteria or
 PT protozoa or to cancer antigens.

XX Disclosure; Page 33; 85pp; English.

XX This invention describes a method in which a secretory IgA-mediated
 CC immune response is elicited in a subject. The method involves
 CC administering to at least 1 mucosal surface of the subject a non-toxic
 CC pseudomonas exotoxin A-like (PE-like) chimeric immunogen comprising a
 CC cell recognition domain of that binds to a cell surface receptor on the
 CC mucosal surface, a translocation domain comprising an amino acid sequence
 CC of PE domain II to effect translocation to a cell cytosol, a foreign
 CC epitope domain comprising an amino acid sequence of that encodes a
 CC foreign epitope, and a sequence encoding an endoplasmic reticulum (ER)
 CC retention domain that comprises an ER retention sequence. Also described
 CC is a composition comprising secretory IgA antibodies that specifically
 CC recognise an epitope of HIV-1. The method can be used for eliciting an
 CC immune response to pathogens, e.g. virus, bacteria or parasitic protozoa
 CC or to a cancer antigen. The antibodies produced can also be isolated and
 CC used, e.g. for affinity chromatography. The PE immunogens can be made by
 CC wholly recombinant techniques which allows insertion of existing variants
 CC of an epitope, or new variants of rapidly evolving epitopes. The PE can
 CC be engineered to alter the function of its domains, thereby providing a
 CC variety of activities, e.g. by replacing the native cell binding domain
 CC of PE A (domain Ia) with a ligand for a particular cell receptor, the
 CC chimera can be targeted to bind to the particular cell type. By providing
 CC a cell recognition domain that binds to a mucosal surface a secretory
 CC immune response involving IgA can be elicited. This sequence represents a
 CC PE protein endoplasmic reticulum (ER) retention domain motif

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 19

AAW85767
 ID AAW85767 standard; peptide; 4 AA.

XX
 AC AAW85767;

XX 27-SRP-1999 (first entry)

XX DE Endomembrane retention signal.

XX KW Targeting molecule; J chain; immunoglobulin; IgM; IgA; substrate;

XX KW epithelial cell; cancer; treatment; therapy;

XX KW non-small cell lung carcinoma; breast carcinoma; colon carcinoma;

XX KW ovarian carcinoma; prostate carcinoma; endometriosis; viral infection;

XX KW inflammation.

XX OS Synthetic.

XX PN WO9920310-A1.

XX PD 29-APR-1999.

XX PF 20-OCT-1998; 98WO-US022304.

XX PR 20-OCT-1997; 97US-00954211.

XX PA (EPIC-) EPICYTE PHARM INC.

XX PI Hein MB, Hiatt AC, Fitchen JH;

XX DR WPI; 1999-288174/24.

XX KW Targeting molecule useful in drug delivery for treating cancer, viral infection or inflammatory disorders.

XX PS Example 1; Page 47; 102pp; English.

XX CC A targeting agent for improving the delivery of drugs to target cells, particularly for delivery of enzymes, binding agents, inhibitors, nucleic acids, carbohydrates and lipids, is new. The targeting agent comprises a polypeptide which forms a closed covalent loop and contains at least three peptide domains having beta-sheet character, each of the domains being separated by domains lacking beta-sheet character. The targeting molecule preferably comprises all or a portion of a native J chain sequence. J chain is a 15 kD protein that, in vivo, links IgM or IgA monomers to form pentameric IgM or dimeric IgA. The polypeptide is linked to at least one biological agent which is capable of entering and killing a non-polarised epithelial cell. The targeting molecule may be linked to the biological agent by a substrate for an intracellular or extracellular enzyme which is associated with or secreted by the non-polarised target cell. The targeting molecule can be used in a pharmaceutical composition for treating a patient afflicted with a disease associated with non-polarised epithelial cells, especially cancer e.g non-small cell lung carcinoma, breast carcinoma, colon carcinoma, ovarian carcinoma, prostate carcinoma and endometriosis, viral infection or inflammatory disorders. This peptide is an endomembrane retention signal which can be attached to the carboxy terminal end of the targeting molecules described

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEEL 4

Db 1 KDEEL 4

RESULT 20

AAAY30052

ID AAY30052 standard; peptide; 4 AA.

XX AC AAY30052;

XX DT 06-OCT-1999 (first entry)

XX DE Organelle targeting domain peptide sequence.

XX KW Multimerisation; chimeric protein; rapamycin compound; gene therapy;

KW transcription; cell growth; cell proliferation; cell differentiation; apoptosis.

XX OS Unidentified.

XX PN WO9936553-A2.

XX PD 22-JUL-1999.

XX PF 15-JAN-1999; 99WO-US000178.

XX PR 15-JAN-1998; 98US-0071591P.

XX PR 21-JAN-1998; 98US-0072016P.

XX PR 22-JAN-1998; 98US-00012097.

XX PR 22-JAN-1998; 98US-0072219P.

XX PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

XX PI Clackson TP, Gilman MZ, Holt DA, Keenan TP, Rozamus L, Yang W;

XX DR WPI; 1999-468986/39.

XX PT Multimerizing chimeric proteins in cells useful in gene therapy, for e.g. target gene transcription and growth of engineered cells.

XX PS Disclosure; Page 56; 155pp; English.

XX CC The specification describes a process for multimerising chimeric proteins in cells. The method comprises forming a complex between a rapamycin compound and cells containing at least one recombinant nucleic acid (rNA) construct encoding specialised chimeric proteins (CPs). The method is used for multimerising chimeric proteins in cells, which is useful for gene therapy, activating the transcription of a desired gene, actuating cell growth, proliferation, differentiation or apoptosis, or triggering other biological events in engineered cells in a rapalog-dependent manner. The present sequence can be included in the chimeric proteins of the invention

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEEL 4

Db 1 KDEEL 4

RESULT 21

AAAY27177

ID AAY27177 standard; peptide; 4 AA.

XX AC AAY27177;

XX DT 15-SEP-1999 (first entry)

XX DE Organelle-targeting domain peptide fragment.

XX KW Drug-induced growth; cell proliferation; cell differentiation; leukemia; signalling domain; drug-binding domain; hemopoietic disease; leukopenia; neurodegenerative disease; thrombocytopenia; beta-thalassemia; sickle cell anemia; Fanconi anemia; myelodysplastic syndrome; chronic granulomatous disease; leukocyte adhesion deficiency.

XX OS Unidentified.

XX PN WO9934836-A1.

XX PD 15-JUL-1999.

XX PF 07-JAN-1999; 99WO-US000348.

PR 08-JAN-1998; 98US-0070754P.
 PR 09-JAN-1998; 98US-0070893P.
 PR 02-OCT-1998; 98US-0102888P.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Blau CA;
 XX
 DR WPI; 1999-430335/36.
 XX
 PT A method to positively select engineered cells and controlling cell
 PT differentiation and growth, useful for expanding subpopulations of cells.
 XX
 PS Disclosure; Page 6; 77pp; English.
 XX
 CC The invention relates to a method for rendering a subpopulation of
 CC mammalian cells susceptible to drug-induced growth, proliferation or
 CC differentiation. The method comprises transducing one or more cells of a
 CC population of primary mammalian cells with at least one recombinant DNA
 CC construct encoding a fusion protein. The fusion protein comprises at
 CC least one signalling domain and at least one drug-binding domain which is
 CC heterologous with respect to the signaling domain and binds to a selected
 CC drug. Exposure of the transduced cells to the drug induces growth,
 CC proliferation or differentiation of the cells. The methods can be used to
 CC expand a subpopulation of primary mammalian (especially human) cells.
 CC This is useful for obtaining populations of megakaryocytes, neutrophils
 CC or erythroid cells. The methods are useful for treating a hemopoietic
 CC disease or pathological condition, or neurodegenerative disease in a
 CC mammal. In particular, the methods can be used for rendering a
 CC subpopulation of human embryonic stem cells susceptible to drug-induced
 CC growth, proliferation or differentiation. The methods are also useful for
 CC administering hemopoietic stem cell therapy to a mammal. Hemopoietic
 CC diseases suitable for treatment include thrombocytopenia, leukopenia,
 CC leukemia, beta-thalassemia, sickle cell anemia, Fanconi anemia, aplastic
 CC anemia, myelodysplastic syndrome, chronic granulomatous disease and
 CC leukocyte adhesion deficiency
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 1 KDEL 4
 RESULT 22
 ID AAY49700
 AC AAY49700 standard; peptide; 4 AA.
 XX
 AC AAY49700;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Pseudomonas exotoxin peptide #4.
 XX
 KW Pseudomonas exotoxin; PE; mutagenised; IL-13; chimeric; interleukin;
 KW cytotoxin; fusion protein; cancer; glioma; neoplasia.
 XX
 OS Synthetic.
 OS Pseudomonas sp.
 XX
 FN WO9951643-A1.
 XX
 PD 14-OCT-1999.
 XX
 XX 31-MAR-1999; 99WO-US007188.
 PF
 XX 03-APR-1998; 98US-00054711.
 PR
 XX (PENN-) PENN STATE RES FOUND.
 PA

XX Debinski W;
 PI
 XX WPI; 1999-633731/54.
 DR
 XX
 PT New mutagenized interleukin 13 molecules for delivery of cytotoxins to
 PT cells over expressing IL13 receptors.
 XX
 PS Disclosure; Page 17; 57pp; English.
 XX
 CC The present invention describes targeting ligands which are mutagenized
 CC IL13 (interleukin 13) molecules having one or more mutations in the
 CC domain that interacts with the hIL14 receptor subunit designated the 140
 CC kDa hIL14beta subunit. A cytotoxic molecule covalently attached to a
 CC mutagenized hIL13 can be used for delivering an effector molecule to a
 CC cell bearing an IL13 receptor. Where the effector molecule is a
 CC cytotoxin, neoplastic cells (e.g. a glioma) can be killed or inhibited.
 CC The methods are used to target effector molecules to kidney cancers, to
 CC skin cancers (Kaposi's sarcoma) and to brain cancers (gliomas and
 CC medulloblastomas). When the mutagenized cell is attached to a detectable
 CC label the chimeric label can be used to detect the presence or absence of
 CC tumour cells, or localize and/or quantify a cell or cells expressing an
 CC IL13 receptor. The label localizes at the site of overexpression and
 CC indicates the presence, absence, quantity or location of such cells. If
 CC the effector molecule is an antibody the chimeric molecule may act to
 CC enhance and direct an immune response toward target cancer cells. The
 CC mutagenized IL13s may be conjugated to a drug such as vinblastine,
 CC doxorubicin, gemistein, an antisense molecule, ribozymes or any other
 CC pharmacological agent to specifically target target cells over expressing
 CC IL13 receptors. The targeting ligands have increased specificity for
 CC cancer cells as compared to normal cells and are therefore very effective
 CC for specifically delivering effector molecules to various neoplasias. The
 CC present sequence is used in the exemplification of the present invention
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 1 KDEL 4
 RESULT 23
 ID AAW96345
 AC AAW96345 standard; peptide; 4 AA.
 XX
 AC AAW96345;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE Endoplasmic reticulum localisation signal peptide.
 XX
 KW Antibody; immune response; modulation; MHC; IRM; receptor; intrabody;
 KW major histocompatibility complex; graft rejection;
 KW immunomodulatory response molecule; regulation; transplantation;
 KW retention signal; localisation signal; golgi apparatus; ER;
 KW endoplasmic reticulum.
 XX
 OS Synthetic.
 OS
 FN WO9914353-A2.
 XX
 PD 25-MAR-1999.
 XX
 XX 18-SEP-1998; 98WO-US019563.
 PF
 XX 19-SEP-1997; 97US-0059339P.
 PR
 XX (DAND) DANA FARBER CANCER INST INC.
 PA
 XX

PT bacteria, or protozoa or to cancer antigens.
XX
PS Claim 13; Page 64; 92pp; English.
XX
CC This invention describes a non-toxic Pseudomonas exotoxin A-like (PE-like) chimeric immunogen. This PE-like immunogen can be used in vaccines and for producing antibodies against the non-native epitope. It can be used for producing an immune response to a pathogen, e.g. a virus, bacteria or parasitic protozoa or a cancer antigen. The antibodies can also be isolated and used for e.g. affinity chromatography. The PE immunogens can be made by wholly recombinant techniques which allows insertion of existing variants of an epitope, or new variants of rapidly evolving epitopes. The PE can be engineered to alter the function of its domains, thereby providing a variety of activities, e.g. by replacing the native cell binding domain of PE A (domain Ia) with a ligand for a particular cell receptor, the chimera can be targeted to bind to the particular cell type. The immunogens can elicit humoral, cell-mediated and secretory immune responses against the non-native epitope. This sequence represents a PE protein endoplasmic reticulum (ER) retention domain motif
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDEL 4
DB 1 KDEL 4
RESULT 25
AAV29637
ID AAY29637 standard; peptide; 4 AA.
XX
AC AAY29637;
XX
XX 20-OCT-1999 (first entry)
XX
XX KDEL peptide for targeting proteins and bearing them to ER.
XX
XX Dimerising agent; regulation; gene transcription; growth; rapamycin; proliferation; differentiation; chimeric protein; FKBP; FRB domain; FK506-binding protein; human FRAP protein; biological response; apoptosis; gene therapy.
XX
XX Unidentified.
XX
XX WO9941258-A1.
XX
XX 19-AUG-1999.
XX
XX 12-FEB-1999; 99WO-US003095.
XX
XX 13-FEB-1998; 98US-0074584P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Schreiber SL, Crabtree GR, Liberles SD;
XX
XX WPI; 1999-508621/42.
XX
XX New C3 substituted rapamycin derivatives acting as dimerization agents for chimeric proteins, used to trigger biological responses, e.g. growth or proliferation, in transformed cells - have minimal immunosuppressant activity.
XX
XX Disclosure; Page 49; 148pp; English.
XX
XX The present invention describes rapamycin derivatives (I) containing the basic substructure and optionally having one or more substituents and unsaturations (between carbons 1 and 8), as pure stereoisomers or their

PI Marasco W, Mhaehikar A;
XX
DR WPI; 1999-229546/19.
XX
PT Altering the regulation of the immune system.
XX
XX Disclosure; Page 27; 56pp; English.
XX
CC Intracellular binding to a desired target by an intracellularly expressed antibody (i.e. an intrabody) can be used to knock out multiple locuses of immunomodulatory receptor molecules (IRMs), so that the expression of multiple major histocompatibility (MHC) molecules is blocked. This selective targeting of IRMs, their pathways or components, can be used to selectively regulate the immune system by controlling expression of these molecules and preventing an undesired immune response in a cell. Any component of the MHC pathway or the MHC assembly line or antigen presentation can be targeted. Intrabodies can be used to knock out the immune response in a particular tissue or portion of the body to prepare it for cell or tissue transplantation. Alternatively, an organ for transplantation can be perfused with the intrabody ex vivo. The intrabodies can comprise whole antibodies, heavy chains, Fab' fragments, single-chain antibodies and diabodies. The intrabodies also comprise an intracellular localisation signal to facilitate interception of expressed proteins. For example, if the target was a cell surface receptor, the antibody would comprise a leader sequence and an endoplasmic reticulum (ER) or Golgi apparatus retention signal. This peptide is an endoplasmic reticulum localisation sequence. For other localisation sequences see AAW96345-W96377
XX
XX Sequence 4 AA;
Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDEL 4
DB 1 KDEL 4
RESULT 24
AAW92925
ID AAW92925 standard; protein; 4 AA.
XX
XX AAW92925;
XX
XX 17-MAY-1999 (first entry)
XX
XX Pseudomonas sp. exotoxin A PE ER retention peptide motif #3.
XX
XX Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen; antibody production; non-native epitope; immune response; antigen; cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated; secretory; ER; endoplasmic reticulum; retention sequence.
XX
XX Pseudomonas sp.
XX
XX WO9902713-A1.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US014341.
XX
XX 11-JUL-1997; 97US-0052375P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fitzgerald DJ;
XX
XX WPI; 1999-120914/10.
XX
XX New Pseudomonas exotoxin chimeric immunogens - comprise a non-native epitope for producing an immune response to pathogens, e.g. virus,

CC mixtures and derivatives. (I) are used to dimerise/multimerise chimeric
 CC proteins that contain domains of the FK506-binding protein, FKBP, and an
 CC FRB domain (from human FRAP protein), so can be used as switches to
 CC trigger selected biological responses, e.g. growth, proliferation,
 CC differentiation, apoptosis and gene transcription, particularly in
 CC conjunction with gene therapy, but also for controlling production or
 CC recombinant proteins and viruses and generally in biological research.
 CC (I) have much lower immunosuppressive activity than known rapamycins,
 CC e.g. 200 times lower, so are safer to use. The present sequence
 CC represents an amino acid sequence which targets proteins bearing them to
 CC the endoplasmic reticulum (ER), given in the present invention

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 26

AAAY25688 standard; protein; 4 AA.

XX AC AAY25688;

XX DT 01-OCT-1999 (first entry)

XX DE Membrane retaining protein leader sequence motif 1.

XX KW SYNVG protein; aggregate; lipid bilayer; beta-glucuronidase; GUS;
 XX KW transmembrane; therapeutic; sequestration; adhesive; membrane retention.

XX OS Unidentified.

XX PN US5935822-A.

XX PD 10-AUG-1999.

XX PF 21-MAR-1995; 95US-00407900.

XX PR 21-MAR-1995; 95US-00407900.

XX PA (COLS) UNIV COLORADO.

XX PI Staehelin A, Giddings T, Galbraith D;

XX DR WPI; 1999-468145/39.

XX PT Aggregating a desired molecule in a lipid bilayer, useful for protective
 XX PT production, directed secretion and in therapy, diagnosis and the
 XX PT biosynthetic production of molecules.

XX PS Disclosure; Col 35-36; 27pp; English.

CC This invention describes novel aggregate molecules (AgM) comprising an
 CC adhesive molecule attached to a desired product molecule. The products of
 CC the invention are used in a method to aggregate a desired product
 CC molecule in a lipid bilayer and comprises forming oligomers between two
 CC or more aggregate molecules that are physically associate with a lipid
 CC bilayer such that the aggregate molecules are accumulated in association
 CC with the lipid bilayer, where the aggregate molecules comprise a beta-
 CC glucuronidase (GUS) adhesive molecule and the desired product molecule is
 CC linked to the adhesive molecule by a transmembrane molecule. The method
 CC can be applied to production of a therapeutic composition. The
 CC sequestration acts to protect the integrity of a product molecule, as
 CC well as to facilitate recovery of the molecule. AAY25688-Y25694 represent
 CC leader sequence motifs which allow the retention of proteins in the
 CC membranes of cells

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 27

AAAY98152

ID AAY98152 standard; peptide; 4 AA.

XX AC AAY98152;

XX DT 22-AUG-2000 (first entry)

XX DE Protein localisation signal sequence.

XX KW Localisation signal; transgenic plant; hydrogen peroxidase production;
 XX KW colorimetric test; oxalate oxidase; pathogen resistance; endo-chitinase.

XX OS Unidentified.

XX PN WO200022148-A1.

XX PD 20-APR-2000.

XX PF 08-OCT-1999; 99WO-FR002412.

XX PR 09-OCT-1998; 98FR-00012704.

XX PA (BIOG-) BIOGEMMA.

XX PI Pagniez M, Grison R, Toppan A;

XX DR WPI; 2000-317998/27.

XX PT Producing transgenic plants expressing a hydrogen peroxide-producing
 XX PT protein, useful for imparting pathogen resistance or as marker for
 XX PT transformation with second gene.

XX PS Disclosure; Page 7; 41pp; French.

XX CC The present sequence represents a protein localisation signal sequence.
 XX CC The peptide can be used in the method of the invention. The invention
 XX CC relates to the production of transgenic plants that express a protein
 XX CC able to produce hydrogen peroxide. The production method comprises
 XX CC transforming a plant cell with Agrobacterium rhizogenes containing a
 XX CC vector that carries a gene encoding the protein to be expressed in the
 XX CC transgenic plant, selection is made for the expression of the gene in a
 XX CC colorimetric test using peroxidase. Plants are transformed to produce a
 XX CC protein of interest, specifically oxalate oxidase (OO): (i) to impart
 XX CC resistance to pathogens (OO degrades oxalic acid, a phytotoxin produced
 XX CC by many phytopathogens); or (ii) as a selection system for plants
 XX CC transformed with a second gene, encoding another protein of interest,
 XX CC introduced in the same vector as the gene encoding the first protein of
 XX CC interest. Particularly the second protein confers resistance to pathogens
 XX CC (fungi, bacteria, insects, nematodes etc.) and is specifically endo-
 XX CC chitinase. The method uses a simple and rapid method, based on a
 XX CC colorimetric test, to select for transformation, particularly using as
 XX CC test sample roots induced by Agrobacterium rhizogenes. It is not
 XX CC necessary that the cells being treated should survive the test, so high
 XX CC (toxic) concentrations of substrate can be used

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 28
ID AAB09912 standard; peptide; 4 AA.
XX
AC AAB09912;
XX
DT 06-NOV-2000 (first entry)
XX
DE Targeting and internalisation signal #3.
XX
KW Targeting signal; MUC-1; immunosuppression; autoimmune disorder;
KW immune disorder; inflammatory disorder.
XX
OS Synthetic.
XX
PN WO200034468-A2.
XX
PD 15-JUN-2000.
XX
PF 09-DEC-1999; 99WO-US029016.
XX
PR 11-DEC-1998; 98US-0111973P.
XX
PA (BIOM-) BIOMIRA INC.
XX
PI Agrawal B, Longenecker BM;
XX
DR WPI; 2000-423418/36.
XX
PT Use of agent capable of intracellularly inhibiting mucin MUC-1 for
PT inducing T-cell-based immunosuppression and for treating autoimmune
PT disorders, transplant rejection and inflammatory disorders.
XX
PS Disclosure; Page 14; 51pp; English.
XX
CC The present sequence is a peptide which forms a targeting domain. The
CC peptide can be used to internalise sequences, such as MUC-1 antagonists,
CC within the cell. MUC-1 is an immunosuppressor, and antagonists act to
CC reduce overactive immune responses. Thus, the peptide can be used to
CC treat inflammatory disorders such as rheumatoid arthritis, psoriasis,
CC allergic contact dermatitis and ankylosing spondylitis, autoimmune
CC disorders including myasthenia gravis, systemic lupus erythematosus,
CC polyarthritis nodosa, Goodpastures syndrome, isopathic thrombocytopenic
CC purpura, autoimmune haemolytic anaemia, Graves' disease, rheumatic fever,
CC pernicious anaemia, insulin-resistant diabetes mellitus, bullous
CC pemphigoid, pemphigus vulgaris, viral myocarditis, autoimmune
CC thyroiditis, male infertility, sarcoidosis, allergic encephalomyelitis,
CC multiple sclerosis, Sjorgens disease, Reiter's disease, Celiac disease,
CC sympathetic ophthalmia and primary biliary cirrhosis, immune disorders,
CC graft versus host disease and transplant rejection

QY Sequence 4 AA;
Best Local Similarity 100.0%; Score 20; DB 3; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 29
ID AAY70697
XX
AC AAY70697 standard; peptide; 4 AA.
XX
PN AAY70697;
XX

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 30
ID AAY56883
XX
AC AAY56883;
XX
DT 14-APR-2000 (first entry)
XX
DE Endoplasmic reticulum (ER) retrieval signal sequence.
XX
KW ER; polypeptide vector; endoplasmic reticulum; retention signal;
KW protease; drug delivery; immune system; glycosylation.
XX
OS Bordetella pertussis.
XX
PN CA2228822-A1.
XX

DT 18-JUL-2000 (first entry)
XX
DE Rat endoplasmic reticulum retention signal peptide.
XX
KW Attractin; immune response; macrophage; monocyte; T cell; cancer; rat;
KW immunostimulant; immunosuppressed patient; immunodeficiency syndrome; ER;
KW transplant; autoimmune disease; endoplasmic reticulum retention signal.
XX
OS Rattus rattus.
XX
PN WO200015651-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-US020948.
XX
PR 14-SEP-1998; 98US-0100137P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Duke-Cohan JS, Schlossman SF;
XX
DR WPI; 2000-271373/23.
XX
PT Isolated nucleic acids encoding human attractin polypeptides useful for
PT enhancing immune responses.
XX
PS Disclosure; Page 30; 120pp; English.
XX
CC The patent discloses four forms of human attractin polypeptides which
CC enhance immune response by promoting macrophage and monocyte spreading in
CC the presence of T cells. These include soluble attractin-1 and -2 and
CC membrane attractin-1 and -2. These various forms of attractin are encoded
CC by alternatively spliced mRNA molecule transcribed from a single gene.
CC The present sequence is a retention signal for endoplasmic reticulum (ER)
CC which can be used to direct attractin to a specified intracellular
CC location. Attractin can be used to enhance immune response in
CC immunosuppressed patients such as those undergoing chemo- and radio-
CC therapy treatment for cancer or those suffering from common variable
CC immunodeficiency syndrome. The protein may also be used to screen
CC modulators (agonists and antagonists) of immune responses which may also
CC be used to regulate immune reactions. Attractin antibodies can be used to
CC inhibit immune response in transplant recipients or patients afflicted
CC with autoimmune disease

QY Sequence 4 AA;
Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 30
ID AAY56883
XX
AC AAY56883;
XX
DT 14-APR-2000 (first entry)
XX
DE Endoplasmic reticulum (ER) retrieval signal sequence.
XX
KW ER; polypeptide vector; endoplasmic reticulum; retention signal;
KW protease; drug delivery; immune system; glycosylation.
XX
OS Bordetella pertussis.
XX
PN CA2228822-A1.
XX

PD 14-OCT-1999.
 XX
 PF 14-APR-1998; 98CA-02228822.
 XX
 PR 14-APR-1998; 98CA-02228822.
 XX
 PA (SALE/) SALEH M T.
 XX
 PI Saleh MT;
 XX
 DR WPI; 2000-127150/12.
 XX
 PT Polypeptide vectors comprising an endoplasmic reticulum retrieval signal
 PT for delivery of drugs and epitopes to the immune system.
 XX
 PS Claim 1; Page 7; 8pp; English.
 CC The invention provides a polypeptide vector, no longer than 69 amino
 CC acids in length that comprises a helix-loop-helix motif, an endoplasmic
 CC reticulum (ER) retention signal (either KDEL and/or RDEL) a protease
 CC recognition sequence subtended by a disulfide bond and glycosylation
 CC site(s). The vector may be used for delivery of drugs and epitopes to the
 CC immune system. The vector is small in size, rigid in structure and can be
 CC modified to optimize it's efficacy of delivery. There is no need for
 CC adjuvants or the need to recruit circulating cells from the immune system
 CC to any specific site as the construct will target cells of the immune
 CC system through the carbohydrate structure in the glycosylation motif. The
 CC vector does not have any specific cytotoxic effects as it has no
 CC cytotoxic enzyme activity. The present sequence represents a ER retrieval
 CC signal used in the vector of the invention
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 31
 AAY32395
 ID AAY32395 standard; peptide; 4 AA.

AC AAY32395;

DT 13-MAR-2000 (first entry)

DE Endoplasmic reticulum retention signal.

KW Endoplasmic reticulum; retention signal; monocotyledonous plant; monocot;
 KW rice; wheat; transgenic plant; mammalian polypeptide; antibody;
 KW expression cassette.

OS Synthetic.

PN WO9966026-A2.

PD 23-DEC-1999.

PF 15-JUN-1999; 99WO-US013584.

PR 15-JUN-1998; 98US-0089322P.

PA (INNE-) INNES CENT JOHN.

PA (CHRI/) CHRISTOU P.

PI Christou P, Stroger E, Fischer R, Martin-Vaquero C, Schillberg S;

PI Ma JK;

XX WPI; 2000-097739/08.

DR

XX Production of mammalian polypeptides, especially antibodies, by
 PT monocotyledonous plants.
 XX
 PS Claim 2; Page 57; 76pp; English.
 XX
 CC This sequence represents an endoplasmic reticulum (ER) retention signal.
 CC Levels of mammalian polypeptide expression in transgenic monocotyledonous
 CC plants can be enhanced by use of this signal. The invention provides
 CC rice, wheat and other monocot plants that have been transformed with
 CC expression cassettes for production of mammalian polypeptides, such as
 CC antibodies. ER retention signals (see also AAY32396), 5' untranslated
 CC regions and leader peptides are employed in various combinations to
 CC provide high expression yield. Plant cell or seed containing polypeptides
 CC selected from Fv, Fab, F(ab)2, diabody, dimeric scFv, whole antibody and
 CC four-chain secretory antibody are claimed. Multi-chain complexes such as
 CC four-chain secretory antibodies are produced by expression of component
 CC polypeptides from separate vectors, all introduced into the same cell by
 CC transformation
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 1 KDEL 4

RESULT 32

AAB03195

ID AAB03195 standard; peptide; 4 AA.

AC AAB03195;

DT 23-OCT-2000 (first entry)

DE Endoplasmic reticulum (ER) localisation signal peptide.

KW ER localisation signal; endoplasmic reticulum; subcellular targeting;
 KW murine; porcine VCAW-specific single chain antibody; sfv; human;
 KW vascular cell adhesion molecule; transgenic animal;
 KW organ transplantation; xenotransplantation;
 KW xenograft rejection suppression.

OS Mus sp.

PN WO200031126-A2.

PD 02-JUN-2000.

PF 22-NOV-1999; 99WO-GB003888.

PR 20-NOV-1998; 98GB-00025555.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Ramrakha PS, George AJT, Haskard D, Lechler RI;

DR WPI; 2000-400039/34.

XX Biological tissue for combating cellular phase of rejection process
 PT resulting from xenotransplantation comprises endothelial cells which may
 PT be induced to generate compound which down-regulates expression of cell
 PT adhesion molecule.

PS Example 2; Page 15; 36pp; English.

XX The invention relates to a biological tissue comprising endothelial cells
 CC which can be induced to generate a compound which downregulates the
 CC expression of a cell adhesion molecule. The invention also encompasses a

CC	polypeptide comprising a region capable of binding a cell adhesion	XX	Gene delivery system, useful for treating or preventing cancer and
CC	molecule, and a subcellular targeting region, a nucleotide sequence	PT	rheumatoid arthritis, comprises receptor-internalized ligand linked to
CC	encoding the polypeptide, and vectors and cells comprising the nucleotide	PT	nucleic acid binding domain and nucleic acid.
CC	sequence. The invention also relates to animals comprising the biological	XX	
CC	tissue of the invention and a method of rendering a tissue or organ	PS	Disclosure; Col 31; 131pp; English.
CC	suitable for transplantation by expressing the cell adhesion molecule-	XX	
CC	binding polypeptide in endothelial cells in the tissue or organ. The cell	XX	
CC	adhesion molecule-binding polypeptide sequesters the cell adhesion	XX	
CC	molecule, thereby reducing cell surface level of the protein and	XX	
CC	preventing the targeting of the transplanted biological tissue by	XX	
CC	signalling proteins involved in the rejection process. The biological	XX	
CC	tissue and methods are useful for combating the cellular phase of the	XX	
CC	rejection process resulting from xenotransplantation, without	XX	
CC	compromising the immune system of the recipient of the grafted tissue. In	XX	
CC	the exemplifications of the invention, a single chain antibody (scFv)	XX	
CC	comprising human VH segments is generated. The scFv is specific for	XX	
CC	porcine VCAM (vascular endothelial cell adhesion molecule) and also	XX	
CC	contains an endoplasmic reticulum (ER) targeting sequence (KDEL;	XX	
CC	AA803195). When the scFv is expressed in porcine endothelial cells, it is	XX	
CC	located in the ER where it binds VCAM. Both molecules are retained in the	XX	
CC	ER and subsequently degraded, thus reducing cell surface VCAM levels. The	XX	
CC	present sequence represents an endoplasmic reticulum (ER) targeting	XX	
CC	sequence from mouse which was incorporated into the porcine VCAM-specific	XX	
CC	scFv	XX	
XX		XX	
SQ	Sequence 4 AA;	SQ	Sequence 4 AA;
	Query Match 100.0%; Score 20; DB 3; Length 4;		Query Match 100.0%; Score 20; DB 3; Length 4;
	Best Local Similarity 100.0%; Pred. No. 2e+06;		Best Local Similarity 100.0%; Pred. No. 2e+06;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KDEL 4	Qy	1 KDEL 4
Db	1 KDEL 4	Db	1 KDEL 4
RESULT 33		RESULT 34	
AA90442		AA969694	
ID	AA90442 standard; peptide; 4 AA.	ID	AA969694 standard; peptide; 4 AA.
AC		AC	AA969694;
XX		XX	
XX		XX	
DT	18-JUL-2000 (first entry)	DT	08-MAY-2000 (first entry)
XX		XX	
DE	Mammalian cytoplasm translocation signal, SEQ ID NO:42.	DE	Mammalian cytoplasmic translocation signal.
XX		XX	
KW	Targetted gene delivery; fibroblast growth factor receptor;	XX	Cytoplasmic translocation signal; mammalian; targeting;
KW	FGFR-binding protein; nucleic acid binding protein;	KW	gene-activated matrix; neuronal therapeutic agent; neurotrophic;
KW	receptor-internalised ligand; cytotoxin; saporin; gene therapy; cytocide;	KW	neurotrophin family; FGF family; TGF-beta inhibitor; guidance factor;
KW	antiproliferative; cancer; melanoma; diabetic retinopathy;	KW	axonal generation; neurodegenerative disease; Alzheimer's disease;
KW	rheumatoid arthritis; restenosis, Dupuytren's contracture; psoriasis;	KW	Parkinson's disease; Huntington's disease.
KW	eczema; nuclear translocation signal; NTS;	XX	
KW	cytoplasmic translocation signal; endosome-disruptive peptide.	XX	
XX		XX	
OS	Mammalia.	OS	Mammalia.
XX		XX	
PN	US6037329-A.	XX	WO9966959-A2.
XX		PN	
PD	14-MAR-2000.	XX	29-DEC-1999.
XX		PD	
XX		XX	
PF	24-SEP-1996; 96US-00718904.	XX	01-JUN-1999; 99WO-US012126.
XX		PF	
XX		XX	
PR	15-MAR-1994; 94US-00213446.	XX	01-JUN-1998; 98US-00088419.
PR	15-MAR-1994; 94US-00213447.	PR	
PR	29-AUG-1994; 94US-00297961.	PR	23-OCT-1998; 98US-00178286.
PR	13-SEP-1994; 94US-00305771.	XX	
PR	16-MAY-1995; 95US-00441979.	XX	
XX		XX	
PA	(SELE-) SELECTIVE GENETICS INC.	XX	
XX		XX	
PI	Chandler LA, Sosnowski BA, Baird JA;	XX	
XX		XX	
XX	WPI; 2000-292008/25.	XX	
DR		XX	

PA (SELE-) SELECTIVE GENETICS INC.
 XX Baird A, Berry M, Logan A, Gonzalez AM;
 XX WPI; 2000-160565/14.
 DR
 XX A gene-activated matrix device comprising a neuronal therapeutic encoding
 PT agent is capable of inducing neuronal axonal generation.
 XX
 XX Disclosure; Page 65; 125pp; English.
 XX
 CC The invention relates to a novel device for promoting neuronal
 CC regeneration or altering neuronal growth, comprising a gene-activated
 CC matrix (GAM). The GAM comprises a biocompatible matrix, and at least one
 CC DNA encoding a neuronal therapeutic product operably linked to a
 CC promoter. The DNA is non-covalently associated with the matrix. The
 CC device may further comprise a targeting agent, which is complexed with or
 CC conjugated to DNA encoding a neuronal therapeutic agent, and which is
 CC capable of binding to a surface receptor of a neuronal or a repair cell.
 CC This targeting agent may also comprise a linker providing a nuclear or
 CC cytoplasmic translocation signal sequence. The invention also encompasses
 CC methods of preparing a GAM for promoting neuronal regeneration and
 CC survival. The neuronal therapeutic agent encoded by the GAM DNA is
 CC capable of inducing neuronal axonal generation or regeneration, and may
 CC include neurotrophic factors which are members of the neurotrophin
 CC or FGF (fibroblast growth factor) families; inhibitors of antagonists of
 CC axonal generation (e.g., transforming growth factor (TGF)-beta
 CC inhibitors); or a guidance factor which promotes defined nerve growth.
 CC The device can be used to transfer the neuronal therapeutic-encoding DNA
 CC into a neuronal cell or repair cell. The device promotes axonal
 CC generation or regeneration without axonal entrapment. The device allows a
 CC neuronal connection to be established or re-established. The methods and
 CC devices of the invention are useful for treatment of neurodegenerative
 CC diseases such as Alzheimer's disease, Parkinson's disease or Huntington's
 CC disease. Direct plasmid DNA transfer from a matrix to a mammalian repair
 CC cell through stimulation of the wound healing process offers a number of
 CC advantages. Firstly, the ease of producing and purifying DNA constructs
 CC compares favourably with traditional protein production method costs.
 CC Secondly, matrices can act as structural scaffolds that promote cell
 CC ingrowth and proliferation. Thirdly, direct gene transfer may be an
 CC advantageous method of delivery for molecules that normally undergo
 CC complex biosynthetic processing or for receptors, which must be properly
 CC positioned in the cell membrane. Sequences AAY69694-Y69696 represent
 CC cytoplasmic translocation signal sequences
 XX
 XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 DB ||||
 1 KDEL 4

RESULT 35
 AAY92046
 ID AAY92046 standard; peptide; 4 AA.
 AC
 XX AAY92046;
 XX
 XX 01-AUG-2000 (first entry)
 DT
 XX Endoplasmic reticulum retention signal sequence.

XX Cyclophilin-like peptidyl prolyl cis-trans isomerase; food processing;
 KW Endoplasmic retention signal; cis-trans isomerization; protein secretion;
 KW toxin; ADP-glucose pyrophosphorylase; glucanase; beta-1,4-endoglucanase.
 XX
 OS Aspergillus niger.
 XX
 PN WO200018934-A1.

XX 06-APR-2000.
 XX 30-SEP-1999; 99WO-IB001669.
 XX 30-SEP-1998; 98GB-00021198.
 XX (DANI-) DANISCO AS.
 XX Derkx PMF, Madrid SM;
 XX WPI; 2000-293167/25.
 XX New peptidyl prolyl cis-trans isomerase, designated CYPB, from
 PT Aspergillus niger, useful in methods for increasing the yield of secreted
 PT polypeptides, such as enzymes used in food processing, from cells.
 XX Claim 8; Page 34; 52pp; English.
 XX
 CC AAY92045-46 are endoplasmic retention (ER) signal sequences found at the
 CC carboxy terminal of polypeptides targeted to the ER in Aspergillus niger.
 CC AAY92047 is a novel ER signal sequence found at the C-terminal end of
 CC CYPB, a cyclophilin-like peptidyl prolyl cis-trans isomerase, also from
 CC A. niger. CYPB is capable of catalyzing the cis-trans isomerization of a
 CC peptide bond on the N-terminal side of proline residues in polypeptides.
 CC CYPB are useful in methods for increasing the yield of secreted
 CC polypeptides from cells. The secreted polypeptides may be enzymes (such
 CC as chymosin, thaumatin or alpha-galactosidase) that can be used in food
 CC processing, a pest toxin, adenosine diphosphate (ADP)-glucose
 CC pyrophosphorylase, a glucanase or beta-1,4-endoglucanase
 XX
 XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 DB ||||
 1 KDEL 4

RESULT 36
 AAY93738
 ID AAY93738 standard; peptide; 4 AA.
 XX
 AC AAY93738;

XX 03-OCT-2000 (first entry)
 DT
 XX Amino acid sequence of a microsomal retention signal.
 DE
 XX Plant expression vector; antigen; hepatitis B surface antigen; HBsAg;
 KW vaccine.
 XX
 OS Unidentified.
 XX
 PN WO200037610-A2.
 XX
 XX 29-JUN-2000.
 XX
 XX 23-DEC-1999; 99WO-US031020.
 XX
 XX 23-DEC-1998; 98US-0113827P.

XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
 PA (HEAL-) HEALTH RES INST.
 XX
 XX Mason HS, Thanavala Y, Arntzen CJ, Richter E;
 XX WPI; 2000-452181/39.
 XX
 PT New expression vector for transforming plants comprising two expression

PT cassettes useful for producing plant material comprising anti-hepatitis B
 XX antibodies.
 PS Disclosure; Page 31; 144pp; English.
 XX The specification describes a plant expression vector which comprises two
 CC expression cassettes, the first comprising a polynucleotide encoding an
 CC antigen and the second comprising a non-identical polynucleotide encoding
 CC the same antigen. The antigen is especially a hepatitis B surface antigen
 CC (HBsAg). The expression vector is used to transform bacterial and plant
 CC cells to elicit the production of anti-hepatitis B antibodies and are
 CC useful as vaccines. The present sequence represents a microsomal
 CC retention signal, which is used in the course of the invention
 XX
 XX Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEL 4
 DB 1 KDEL 4
 RESULT 37
 AAB30285
 ID AAB30285 standard; peptide; 4 AA.
 AC AAB30285;
 XX
 XX 12-FEB-2001 (first entry)
 DT
 DE CD4+ T-cell activation methods peptide ligand #47.
 XX CD4+ T-cell activation; peptide epitope; autoimmune disease;
 KW infectious disease; cancer; immunological mass fingerprinting.
 KW
 XX Synthetic.
 OS
 XX WO200063702-A1.
 PN
 XX 26-OCT-2000.
 PD
 XX 20-APR-2000; 2000WO-US010888.
 PF
 XX 21-APR-1999; 99US-00295868.
 PR
 XX 21-APR-1999; 99US-0130355P.
 PR
 XX (ZYCO-) ZYCO INC.
 PA (UNLO) KINGS COLLEGE LONDON.
 PA
 XX Peakman M, Chicx RM;
 PI
 XX WPI; 2000-665270/64.
 DR
 XX Identifying a class II major histocompatibility complex-binding fragment
 PT of a polypeptide useful for diagnosing and protecting against diabetes
 PT comprises contacting a ligand, a polypeptide and a mammalian antigen
 PT presenting cell.
 PS Disclosure; Page 63; 118pp; English.
 XX The present invention is concerned with a method, designated
 CC immunological mass fingerprinting, which enables the identification of
 CC peptide epitopes that activate CD4+ T-cells. Peptides of this kind are
 CC also given. CD4+ cells are involved in the pathogenesis of disease, and
 CC the peptides can be used in the prevention and treatment of autoimmune
 CC diseases such as diabetes, multiple sclerosis, rheumatoid arthritis,
 CC myasthenia gravis, systemic lupus erythematosus, autoimmune premature
 CC ovarian failure, Graves' thyroiditis, Hashimoto's thyroiditis, primary
 CC hypothyroidism, coeliac disease, primary biliary cirrhosis, autoimmune
 CC hepatitis, Addison's disease, vitiligo, systemic sclerosis and anti-

CC glomerular basement membrane disease, infectious diseases including
 CC leprosy, measles, hepatitis C, HIV and parasitic diseases, and cancer
 XX
 XX Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEL 4
 DB 1 KDEL 4
 RESULT 38
 AAB35117
 ID AAB35117 standard; peptide; 4 AA.
 XX
 XX AAB35117;
 XX
 XX 11-SEP-2003 (revised)
 DT 27-MAR-2001 (first entry)
 DE Adenovirus E3/19K protein.
 XX
 XX Drug resistance mechanism; multi-drug resistance; MDR; cancer;
 KW chemotherapeutic drug.
 KW
 XX unidentified adenovirus.
 OS
 XX WO200072008-A2.
 PN
 XX 30-NOV-2000.
 PD
 XX 25-MAY-2000; 2000WO-US014812.
 PF
 XX 25-MAY-1999; 99US-0136018P.
 PR
 XX (RIGE-) RIGEL PHARM INC.
 PA
 XX Xu X;
 PI
 XX WPI; 2001-025195/03.
 DR
 XX Screening multi-drug resistance conferring polypeptides involves
 PT expressing library of retroviral vectors encoding randomized candidate
 PT peptides and selecting cells expressing MDR phenotype conferred by
 PT peptide.
 XX
 XX Disclosure; Page 19; 73pp; English.
 PS
 XX The present invention provides a method for screening for a peptide which
 CC confers multi-drug resistance (MDR) on a cell. This involves expressing a
 CC library of retroviral vectors encoding randomized candidate peptides in
 CC cells and screening for those peptides which cause a multi drug resistant
 CC phenotype. This method is particularly useful in identifying treatments
 CC for multi-drug resistant cancer. (Updated on 11-SEP-2003 to standardise
 CC OS field)
 XX
 XX Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEL 4
 DB 1 KDEL 4
 RESULT 39
 AAG67291
 ID AAG67291 standard; peptide; 4 AA.

XX AC AAG67291;
 XX 13-NOV-2001 (first entry)
 XX Amino acid sequence of an endoplasmic reticulum retention signal.
 XX hb7-H2; T cell stimulator; immunosuppression; cancer; AIDS;
 KW congenital immune deficiency; cellular immune response;
 KW inflammatory condition; autoimmune disease; rheumatoid arthritis;
 KW multiple sclerosis; insulin-dependent diabetes mellitus.
 XX Unidentified.
 XX WO200164704-A1.
 XX 07-SEP-2001.
 XX 02-MAR-2001; 2001WO-US006769.
 XX 02-MAR-2000; 2000US-0186519P.
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 XX Chen L;
 XX WPI; 2001-514837/56.
 XX An isolated DNA encoding a hb7-H2 polypeptide, useful for treating
 PT cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis, multiple
 PT sclerosis or insulin-dependent diabetes mellitus).
 XX Disclosure; Page 21; 50pp; English.
 XX The specification describes polypeptide, designated hb7-H2. The hb7-H2
 CC polypeptide co-stimulates T cells. The hb7-H2 proteins and its variants
 CC are generally useful as immune response-stimulating therapeutics. For
 CC example, the polypeptides can be used for treatment of disease conditions
 CC characterized by immunosuppression, e.g., cancer, AIDS or AIDS-related
 CC complex, other virally or environmentally-induced conditions, and certain
 CC congenital immune deficiencies. They may also be employed to increase
 CC immune function that has been impaired by the use of radiotherapy or
 CC immunosuppressive drugs such as certain chemotherapeutic agents, and
 CC therefore are particularly useful when given in conjunction with such
 CC drugs or radiotherapy. The hb7-H2 nucleic acid and polypeptide can be
 CC used to treat conditions involving cellular immune responses, e.g.,
 CC inflammatory conditions (such as, for example, those induced by
 CC infectious agents including Mycobacterium tuberculosis or M. leprae), or
 CC other pathologic cell-mediated responses such as those involved in
 CC autoimmune diseases (e.g. rheumatoid arthritis), multiple sclerosis, or
 CC insulin-dependent diabetes mellitus). AAG67288-91 can be used to direct
 CC hb7-H2 to specific intracellular compartments
 XX
 XX Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 1 KDEL 4
 RESULT 40
 AAG78315
 ID AAG78315 standard; protein; 4 AA.
 XX AAG78315;
 XX 11-SEP-2003 (revised)
 DT 15-NOV-2001 (first entry)
 XX

DE ER lumen retention signal.
 XX Proridin; ricin; A chain; B chain; L domain; ER lumen retention signal;
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
 KW retroviral infection; anti-HIV; virucide activity; viral protease.
 XX Unidentified.
 XX WO200160393-A1.
 XX 23-AUG-2001.
 XX 15-FEB-2001; 2001WO-US005282.
 XX 16-FEB-2000; 2000US-0182759P.
 XX (BECH-) BECHTEL BWXT IDAHO LLC.
 XX Keener WK, Ward TE;
 XX WPI; 2001-581908/65.
 XX Novel composition comprising toxin e.g., ricin based antiviral compound
 PT useful for treating viral infections such as human immunodeficiency virus
 PT infection.
 XX Example 6; Page 64; 66pp; English.
 XX The sequence relates to the amino acid sequence of an ER lumen retention
 CC signal fused to ricin A chain in order to enhance its toxicity. The
 CC invention relates to a novel toxin (e.g., ricin) based antiviral agent
 CC which is toxic to virus-infected cells, but non-toxic to uninfected
 CC cells. The invention has anti-HIV and virucide activities. Its mechanism
 CC of action is through inactivation of cellular ribosomes and enhancement
 CC of binding of the antiviral agent to galactose residues on cell surfaces,
 CC and its cellular internalisation. The invention is useful for treating
 CC human immunodeficiency virus infection and other viral infections,
 CC especially retroviral infections. The antiviral agent is activated in
 CC viral particles or early-stage infected cells, killing the cells upon
 CC infection and effectively preventing the integration of the viral genome
 CC into the host genome thereby preventing the latency/rebound problem. The
 CC agent enters all HIV susceptible cells, and not just cells known to act
 CC as host cells for the virus. The antiviral agent remains inert in a cell
 CC until degraded in it, unless the cell is infected with the virus, where
 CC the viral protease activates it. (Updated on 11-SEP-2003 to standardise
 CC OS field)
 XX
 XX Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 1 KDEL 4
 RESULT 41
 AAB45947
 ID AAB45947 standard; peptide; 4 AA.
 XX AAB45947;
 XX 02-APR-2001 (first entry)
 DT Transdominant effector peptide associated screening peptide #27.
 DE Intracellular transdominant bioactive agent; screening; cell phenotype;
 KW effector peptide.
 XX Unidentified.
 XX

PN US6153380-A.
 XX 28-NOV-2000.
 XX 23-JAN-1997; 97US-00789333.
 XX 23-JAN-1996; 96US-00589108.
 PR 23-JAN-1996; 96US-00589911.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (RIGE-) RIGEL PHARM INC.
 XX Rothenberg SM, Nolan GP;
 PI WPI; 2001-060084/07.
 XX Methods for screening intracellular transdominant effector peptides and
 PT RNA molecules comprise delivering random oligonucleotides to cells, which
 PT are then screened for an altered phenotype.
 XX Disclosure; Col 67-68; 57pp; English.
 XX This invention describes novel in vitro screening methods (I) for a
 CC transdominant intracellular bioactive agent capable of altering the
 CC phenotype of a cell. (I) comprises: (a) introducing a molecular library
 CC of randomized candidate nucleic acids into several cells; and (b)
 CC screening the cells for a cell exhibiting an altered phenotype, where the
 CC altered phenotype is due to the presence of a transdominant bioactive
 CC agent. The methods are particularly useful for screening intracellular
 CC transdominant effector peptides and RNA molecules selected inside living
 CC cells from randomized pools. (I) is also useful for introducing random
 CC libraries into cells to screen for bioactive compounds. The methods allow
 CC rapid and highly efficient screening of large numbers of random
 CC oligonucleotides and their corresponding expression products in a single
 CC step. In addition, the methods allow screening in the absence of
 CC significant prior characterization of the cellular defect
 XX Sequence 4 AA;
 SQ Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 1 KDEL 4
 RESULT 42
 AAB96038
 ID AAB96038 standard; peptide; 4 AA.
 XX AAB96038;
 AC AAB96038;
 XX 25-JUN-2001 (first entry)
 DT Endoplasmic reticulum retention signal peptide SEQ ID 111.
 DE Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;
 KW human papillomavirus-associated disease; condyloma; cervical dysplasia;
 KW cervical dysplasia; major histocompatibility complex; MHC I.
 XX Unidentified.
 OS WO200119408-A1.
 PN 22-MAR-2001.
 XX 18-SEP-2000; 2000WO-US025559.
 PF 16-SEP-1999; 99US-00398534.
 PR 16-SEP-1999; 99US-0154665P.
 PR 09-DEC-1999; 99US-00458173.

PR 09-DEC-1999; 99US-0169846P.
 XX (ZYCO-) ZYCOS INC.
 PA Hedley ML, Urban RC, Chicz RM;
 PI WPI; 2001-265996/27.
 XX Novel nucleic acids encoding polypeptide polypeptides containing multiple
 PT epitopes from one or more proteins, useful for treating tumors and as
 PT vaccines against pathogenic agents.
 XX Disclosure; Page 25; 64pp; English.
 XX This invention relates to polynucleotides encoding a hybrid polypeptide
 CC comprising a signal sequence and three segments that are either
 CC contiguous or separated by a spacer amino acid or spacer peptide. The
 CC invention specifically details polynucleotides encoding a polypeptide
 CC peptide where the peptide segments are tumour antigens or a naturally
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit
 CC antiviral and immunostimulatory activity. The polynucleotide and
 CC polypeptide peptides are useful for eliciting an immune response in a
 CC mammal. The polynucleotide and protein are useful as vaccines for
 CC treating tumours and pathogenic infections. The polynucleotide is also
 CC useful for preventing or treating human papillomavirus (HPV)-associated
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV
 CC infection, cervical dysplasia, high grade squamous intraepithelial
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are
 CC useful for generating or enhancing prophylactic or therapeutic immune
 CC response against pathogens, tumours or autoimmune diseases in a
 CC population of individuals having diverse MHC allotypes, as positive
 CC controls in T cell stimulation assays in vitro, and as tools to
 CC understand processing of epitopes within cells. Peptides AAB95994 -
 CC AAB96037 and AAB96044 - AAB96048 represent major histocompatibility
 CC complex I (MHC I) associated tumour and pathogen antigens. The peptides
 CC can be used as part of the polypeptide proteins of the invention. Also
 CC included are examples of the polypeptide proteins represented by AAB96050
 CC - AAB96052, and localisation signal peptides AAB96038 - AAB96043 and
 CC AAB96049 which can be used in the construction of the polypeptide
 CC peptides
 XX Sequence 4 AA;
 SQ Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 1 KDEL 4
 RESULT 43
 AAB70755
 ID AAB70755 standard; peptide; 4 AA.
 XX AAB70755;
 AC AAB70755;
 XX 17-MAY-2001 (first entry)
 DT Endoplasmic reticulum re-import transport protein motif.
 DE Cell membrane transport; compartment transport; transport protein;
 KW membrane-specific transport; gene therapy.
 XX Unidentified.
 OS DE19933492-A1.
 PN 18-JAN-2001.
 XX 16-JUL-1999; 99DE-01033492.
 PF

XX PR 16-JUL-1999; 99DE-01033492.
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX PI Braun K, Friedrich E, Waldeck W, Peschke P, Pipkorn R, Debus J;
 XX WPI; 2001-235973/25.
 XX DR New conjugates for mediating cell, compartment or membrane-specific
 XX PT transport, comprising transport mediator, specific address protein or
 XX PT peptide and active agent, useful in therapy or diagnosis, e.g. gene
 XX PT therapy.
 XX PS Disclosure; Page 3; 10pp; German.
 XX CC This invention describes a novel conjugate (I) for mediating cell-,
 XX CC compartment- or membrane-specific transport, comprising a transport
 XX CC mediator for the cell membrane, a cell-, compartment- or membrane-
 XX CC specific address protein or peptide, and an active agent to be
 XX CC transported. The method also describes the preparation of (I) which
 XX CC comprises (a) separate peptide synthesis of the transport protein,
 XX CC address protein, and optionally a spacer (preferably by Merrifield
 XX CC synthesis); (b) covalent coupling of the address protein to an active
 XX CC agent, optionally via a spacer; and (c) redox coupling of the product of
 XX CC (b) with the transport protein, preferably in aqueous dimethylsulfoxide
 XX CC solution, the product is purified, especially by high performance liquid
 XX CC chromatography (HPLC). The products of the invention can be used for cell
 XX CC -, compartment- or membrane-specific transport of the active agent, in
 XX CC diagnosis and/or therapy. (I) is useful in gene therapy, where a whole
 XX CC gene (including the regulatory elements) can be transported. Targeting
 XX CC using (I) is widely applicable and highly effective. (I) have low
 XX CC immunogenicity, minimal risk of infection and a long duration of action.
 XX CC The specific transportation of the active agent to the required cell
 XX CC compartment gives improved diagnostic or therapeutic results, including
 XX CC reduced side-effects, in human or veterinary medicine
 XX SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db ||||
 1 KDEL 4
 RESULT 44
 AAB20214
 ID AAB20214 standard; peptide; 4 AA.
 XX AC AAB20214;
 XX DT 14-MAY-2001 (first entry)
 XX DE Endoplasmic reticulum retention peptide.
 XX KW Endoplasmic reticulum retention peptide; human papilloma virus; HPV;
 XX KW immunogen; E7 protein; vaccine; infection; gene therapy;
 XX KW exophytic condyloma; flat condyloma; cervical cancer;
 XX KW respiratory papilloma; conjunctival papilloma; cervical dysplasia.
 XX OS Unidentified.
 XX PI US6183746-B1.
 XX PN 06-FEB-2001.
 XX PD 09-OCT-1998; 98US-00169425.
 XX PF 09-OCT-1997; 97US-0061657P.
 XX PR

PA (ZYCO-) ZYCOS INC.
 XX Urban RG, Chicz RM, Collins EJ, Hedley ML;
 XX WPI; 2001-190939/19.
 XX DR Inducing an immune response in a mammal for prophylaxis and treatment of
 XX PT human papilloma virus infections such as cervical cancer, comprises
 XX PT administering immunogenic peptides from the papilloma virus type 16 E7
 XX PT protein.
 XX PS Disclosure; Col 4; 23pp; English.
 XX CC The present sequence is that of an endoplasmic reticulum retention
 XX CC peptide. Claimed methods of the invention involve the administration to a
 XX CC mammal, such as a human, of a nucleic acid encoding a polypeptide
 XX CC comprising a first peptide, which controls intracellular trafficking,
 XX CC e.g. the present sequence, and a second peptide, which is derived from
 XX CC human papilloma virus type 16 E7 protein and which contains multiple
 XX CC overlapping class I HLA-binding T-cell epitopes. The immunogenic peptides
 XX CC and nucleic acids of the invention are used as vaccines prophylactically
 XX CC or therapeutically in subjects having, suspected of having, or at risk of
 XX CC exophytic condyloma, flat condyloma, cervical cancer, respiratory
 XX CC papilloma, conjunctival papilloma, genital-tract HPV infection and
 XX CC cervical dysplasia (claimed)
 XX SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db ||||
 1 KDEL 4
 RESULT 45
 AAB31370
 ID AAB31370 standard; peptide; 4 AA.
 XX AC AAB31370;
 XX DT 20-APR-2001 (first entry)
 XX DE Amino acid sequence of an endoplasmic reticulum retaining peptide.
 XX KW Protein production; food processing; protein antibiotic; feed enzyme;
 XX KW endoplasmic reticulum retaining peptide.
 XX OS Unidentified.
 XX PN WO200077174-A1.
 XX PD 21-DEC-2000.
 XX XX 07-JUN-2000; 2000WO-IL000330.
 XX PF 10-JUN-1999; 99US-00329234.
 XX PR (CBDT-) CBD TECHNOLOGIES LTD.
 XX PA (VISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX PI Shani Z, Shoseyov O;
 XX WPI; 2001-112219/12.
 XX DR Expressing and isolating recombinant protein in a plant, useful for
 XX PT producing large quantities of recombinant proteins, by expressing a
 XX PT fusion protein including a cellulose binding peptide fused to a
 XX PT recombinant protein.
 XX PS Disclosure; Page 41; 87pp; English.

XX The specification describes a method for expressing and isolating a
CC recombinant protein in a plant. The method comprising expressing a fusion
CC protein including the recombinant protein and a cellulose binding peptide
CC fused to it, where the fusion protein is compartmentalised and
CC sequestered within plant cells, plant derived tissue or cultured plant
CC cells. The method is useful for obtaining large quantities of the
CC recombinant proteins and protein products in a simple and cost-effective
CC manner. Recombinant proteins may be used commercially, such as in the
CC food processing industry, e.g. glucosylases and glucose isomerases are
CC used for converting starch to high fructose corn syrup, proteinases for
CC the hydrolysis of high molecular weight proteins and in manufacturing
CC leather or alcoholic beverages, pectinesterases for pectin hydrolysis in
CC food industry, lipases for cleaving ester linkage in triglycerides, and
CC for effluent treatment. The recombinant proteins may further be used to
CC produce protein antibiotics, which can be used in healing processes, and
CC to produce animal feed enzymes. The present sequence represents an
CC endoplasmic reticulum retaining peptide, which is used to produce the
CC fusion proteins of the inventions

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB ||||
1 KDEL 4

RESULT 46
AAU03564
ID AAU03564 standard; peptide; 4 AA.
AC AAU03564;
XX 26-SEP-2001 (first entry)
DT Peptide retention signal for ER.
DE Human; immunoregulatory protein; B7-H1; co-stimulating T-cell;
XX B-cell antibody-producing response; IgG2a antibody response; APC;
KW immunodeficiency disease; inflammatory disease; autoimmune disease;
KW endoplasmic reticulum; ER.
XX Homo sapiens.
OS
XX WO200139722-A2.
PN
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US032583.
PF
XX 30-NOV-1999; 98US-00451291.
PR
XX 28-AUG-2000; 2000US-00649108.
PR
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA
XX Chen L;
XX WPI; 2001-397926/42.
DR
XX Novel DNA encoding immunoregulatory molecule B7-H1, is useful for co-
XX stimulating a T cell for augmenting immunoregulation and for controlling
PT pathologic cell mediated conditions.
PT
XX Disclosure; Page 25; 85pp; English.
PS
XX The present sequence represents the peptide retention signal for the
CC endoplasmic reticulum (ER). The present sequence is described relating to
CC the invention of novel human and mouse immunoregulatory protein B7-H1
CC (AAU03559, AAU03560). B7-H1 is useful for co-stimulating T-cells such as

CC helper T-cells that provide helper activity for B-cell antibody-producing
CC response e.g. IgG2a antibody response, in a mammal having an
CC immunodeficiency disease, inflammatory condition or an autoimmune
CC disease, by culturing B7-H1 with the mammalian T-cells in vitro, or
CC administering B7-H1 or a nucleic acid encoding B7-H1 to the T-cells, such
CC that the level of CD40 ligand on the T-cell surface is increased. The
CC method further involves providing a recombinant cell e.g. an antigen
CC presenting cell (APC) which is the progeny of a cell obtained from the
CC mammal and has been transfected or transformed ex vivo with a nucleic
CC acid encoding B7-H1, so that the cell expresses B7-H1, and administering
CC the cell to the mammal. Prior to administration, the APC is pulsed with
CC an antigen or an antigenic peptide. B7-H1 can be used to control
CC pathologic cell mediated conditions (e.g. those induced by infectious
CC agents such as Mycobacterium tuberculosis) or other pathologic cell
CC mediated responses such as those involved in autoimmune diseases (e.g.
CC rheumatoid arthritis)

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB ||||
1 KDEL 4

RESULT 47
AAB84355
ID AAB84355 standard; protein; 4 AA.
AC AAB84355;
XX 22-AUG-2001 (first entry)
DT Amino acid sequence of an endoplasmic reticulum retention peptide.
DE Surface receptor-dependent infection; pathogenic agent; antibody.
XX Synthetic.
OS
XX WO200142308-A2.
PN
XX 14-JUN-2001.
PD
XX 08-DEC-2000; 2000WO-EP012419.
PF
XX 08-DEC-1999; 99US-0169653P.
PR
XX (NOVS) NOVARTIS AG.
PA (SCRI) SCRIPPS RES INST.
XX Barbas CF, Steinberger P;
PI WPI; 2001-381649/40.
XX
XX Inhibiting, preventing or treating pathogenic infection of cells
PT comprises expressing recombinant antibody specific for surface receptor
PT of cells necessary for pathogenic infection, fused to intracellular
PT anchor means.
XX Claim 5; Page 51; 69pp; English.
PS
XX The specification describes a method for inhibiting, diminishing,
CC preventing or treating surface receptor-dependent infection of cells by
CC pathogenic agents. The method comprises a recombinant antibody protein
CC fused to an intracellular anchor means, where the antibody is specific
CC for a surface receptor of the cells necessary for pathogenic infection.
CC The anchor means may be an endoplasmic reticulum retention peptide. The
CC present sequence represents an endoplasmic reticulum retention peptide,
CC which is used to produce antibody proteins of the invention

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 DB ||||
 1 KDEL 4

RESULT 48
 ABG99144
 ID ABG99144 standard; peptide; 4 AA.
 XX
 AC ABG99144;
 XX
 DT 14-JAN-2003 (first entry)
 XX
 DE Calreticulin endoplasmic reticulum sequence.

Intein; intein-catalysed cyclic peptide library; cancer; tumour cell;
 cardiovascular disease; obesity; neurological disorder; apoptosis;
 cell death; cell division; cell growth; arrhythmia potential;
 cardiomyocyte; heart failure; sarcolemmal calcium cycling; stroke;
 cell proliferation; atherosclerosis; metabolism; skin disorder;
 bone morphogenetic protein; endocrinology; infectious disease;
 viral infection; bacterial infection; diabetic ulcer; wound healing;
 keloid formation; skin connective tissue cell; antibiotic transport;
 drug resistance; cycostatic; anorectic; neuroprotective; cardiac;
 haemostatic; nuclear localisation signal; targeting signal;
 secretory signal.

Unidentified.
 WO200166565-A2.
 13-SEP-2001.
 06-MAR-2001; 2001WO-US007162.
 06-MAR-2000; 2000US-0187130P.
 (RIGE-) RIGEL PHARM INC.
 Kinsella TM;
 WPI; 2001-589926/66.

Fusion polypeptide for generating libraries of cyclic peptides in vivo,
 comprises terminal intein motifs and a random peptide.

Disclosure; Page 20; 115pp; English.

The present invention relates to methods and compositions utilising
 inteins to generate libraries of cyclic peptides in vivo. The
 compositions of the invention are useful for making cyclic peptides in
 vivo. Libraries of cells can be transformed with libraries of fusion
 nucleic acids. Intein-catalysed cyclic peptide libraries are useful for
 screening for an altered phenotype and identifying target molecules. The
 library is introduced into a cell, screened for an altered phenotype and
 target molecules that bind to the cyclic peptide are isolated. The method
 is useful for making cyclic peptides which retain biological activity,
 and for screening for cyclic peptides capable of altering the phenotype
 of a cell. The cyclic peptides are useful for altering cellular
 phenotypes and/or physiology, in screening assays to identify target
 molecules associated with changes in cellular phenotype or physiology and
 as drugs to treat a number of disease state, such as cancer,
 cardiovascular diseases, obesity and neurological disorders. The
 bioactive cyclic peptide is useful as the starting point for
 designing/synthesising derivative molecules with similar or more
 favourable properties for use as a drug and to pull out target molecules.
 By introducing random libraries into any tumour cell, peptides which

CC induce apoptosis, cell death, loss of cell division or decreased cell
 CC growth can be identified and this method is useful in cancer
 CC applications. The methods are also useful in cardiovascular applications,
 CC to screen for diminished arrhythmia potential in cardiomyocytes, for
 CC enhanced contractile properties of cardiomyocytes and diminish heart
 CC failure potential and to identify agents that regulate the intracellular
 CC and sarcolemmal calcium cycling in cardiomyocytes to prevent arrhythmias
 CC and agents that diminish embolic phenomena in arteries and arterioles
 CC leading to stroke. Candidate bioactive peptide libraries are inserted
 CC into these cell types and their proliferation in response to specific
 CC stimuli is monitored. Furthermore, the methods are also useful in
 CC screening for decreases in atherosclerosis, in screens to regulate
 CC obesity by controlling food intake mechanisms or reducing the responses
 CC of the receptor signalling pathways that regulate metabolism, in
 CC neurobiology applications, to screen for agonists of bone morphogenetic
 CC proteins, in skin biology applications, endocrinology applications,
 CC infectious disease applications including viral and bacterial infection,
 CC to screen for cyclic peptides which block HIV-1 infection, regulation or
 CC inhibition of keloid formation and wound healing for diabetic ulcers.
 CC Candidate libraries are inserted into skin connective tissue cells and
 CC bioactive peptides which promote the growth of these cells are isolated.
 CC Further applications include screening for bioactive peptides that block
 CC antibiotic transport mechanisms, drug toxicities and drug resistance,
 CC improving the performance of existing or developmental drugs, and in
 CC biotechnology. ABG99123-ABG99153 represent various targeting signals that
 CC may be fused to intein motifs or peptides
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 DB ||||
 1 KDEL 4

RESULT 49
 AAB48315
 ID AAB48315 standard; peptide; 4 AA.
 XX
 AC AAB48315;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Endoplasmic reticulum retaining peptide.

Recombinant; fusion protein; cellulose binding peptide; CBP; cellulose;
 food industry; alcoholic beverage; hydrolysis; whey lactose; aspartame;
 artificial sweetener; milk; animal feed enzyme; heparin; heparan sulfate;
 protein fiber; effluent treatment; detergent; leather;
 endoplasmic reticulum.

Unidentified.
 OS
 XX
 PN WO200077175-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013434.
 XX
 PR 10-JUN-1999; 99US-00329234.
 XX
 PA (CBDT-) CBD TECHNOLOGIES LTD.
 PA (YISS) YISSUM RES & DEV CO.
 PA (FRIE/) FRIEDMAN M M.
 XX
 PI Shani Z, Shoseyov O;
 XX
 DR WPI; 2001-080683/09.
 XX
 PT Expressing and isolating recombinant protein from plant e.g for use in

PT food industry, involves homogenizing a plant expressing fusion protein
PT including recombinant protein and cellulose binding peptide being fused
PT to it.
XX
PS Disclosure; Page 44; 64pp; English.
XX
CC The invention relates to a process of expressing a recombinant protein in
CC a plant and isolating the recombinant protein from the plant. The method
CC comprises: (a) providing a plant, a plant derived tissue or cultured
CC plant cells expressing a fusion protein (FP) including a recombinant
CC protein and a cellulose binding peptide (CBP) being fused to it, FP being
CC compartmentalized so as to be sequestered from the cell walls; (b)
CC homogenizing the plant, plant derived tissue or cultured plant cells such
CC that FP is brought into contact with a plant derived cellulosic matter
CC (CM) to effect affinity binding of FP via CBP to CM and forming a FP-CM
CC complex; and (c) isolating the FP-CM complex. The recombinant protein
CC isolated by this method is useful commercially in the food industry, for
CC the hydrolysis of high molecular weight protein, in the manufacture of
CC alcoholic beverages, for the hydrolysis of whey lactose, in the
CC production of the artificial sweetener aspartame, in the reduction of the
CC cooked flavor of milk, in the production of animal feed enzymes, in the
CC sterilization and oxidation of plastics and rubbers, for the production
CC of heparin and heparan sulfate oligosaccharides, for purification in
CC industrial processes, for production of protein fibers, for effluent
CC treatment, in combination with detergents in cleaning applications, and
CC in leather manufacturing processes. The present sequence represents a
CC endoplasmic reticulum retaining peptide
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 50
AAB50814
ID AAB50814 standard; peptide; 4 AA.
XX
AC AAB50814;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human endoplasmic reticulum localisation sequence.
XX
KW Fluorescent protein indicator; green fluorescent protein; GFP;
KW linker moiety; sensor; calmodulin-binding domain.
XX
OS Homo sapiens.
XX
FN WO2000071565-A2.
XX
PD 30-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013694.
XX
PR 21-MAY-1999; 99US-00316919.
PR 21-MAY-1999; 99US-00316920.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tsien RY, Baird GA;
XX
DR WPI; 2001-032017/04.
XX
XX Novel fluorescent proteins comprising a sensor protein inserted into
PT them, useful for measuring the response of a sensor biological, chemical,
PT electrical or physiological parameter in vivo or in vitro.
XX

PS Disclosure; Page 32; 94pp; English.
XX
CC The present sequence is a localisation signal sequence used in the
CC construction of a fluorescent protein indicator. The indicator comprises
CC a sensor polypeptide that is responsive to a chemical, biological,
CC electrical or physiological parameter, and a fluorescence protein
CC functional group. The sensor polypeptide is operatively inserted into the
CC fluorescent moiety. The fluorescent indicator is useful for detecting the
CC presence of a response inducing member in a sample. The method involves
CC contacting the sample with the indicator and detecting a change in
CC fluorescence, in which a change is indicative of the effect of the
CC parameter on the sensor polypeptide. The novel fluorescent proteins are
CC advantageous due to their reduced size as compared to the FRET
CC (fluorescence resonance energy transfer)-based sensors
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

Search completed: March 20, 2006, 07:52:21
Job time : 83.5 secs

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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:51:44 ; Search time 18.5 Seconds
(without alignments)
17.876 Million cell updates/sec

Title: US-09-673-707-9
Perfect score: 20
Sequence: 1 KDEL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCJUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	1 US-08-328-961-6	Sequence 6, Appli
2	20	100.0	4	1 US-07-872-673B-5	Sequence 5, Appli
3	20	100.0	4	1 US-08-405-615-16	Sequence 16, Appl
4	20	100.0	4	1 US-08-331-398A-51	Sequence 51, Appl
5	20	100.0	4	1 US-08-462-397-6	Sequence 6, Appli
6	20	100.0	4	1 US-08-270-314-3	Sequence 3, Appli
7	20	100.0	4	1 US-08-406-192-28	Sequence 28, Appl
8	20	100.0	4	1 US-08-082-269D-7	Sequence 7, Appli
9	20	100.0	4	1 US-08-593-865-1	Sequence 1, Appli
10	20	100.0	4	1 US-08-461-234-16	Sequence 16, Appl
11	20	100.0	4	1 US-08-480-190-152	Sequence 152, App
12	20	100.0	4	1 US-08-545-151-28	Sequence 28, Appl
13	20	100.0	4	1 US-08-373-190-17	Sequence 17, Appl
14	20	100.0	4	1 US-08-463-480-16	Sequence 16, Appl
15	20	100.0	4	1 US-08-470-566B-51	Sequence 51, Appl
16	20	100.0	4	1 US-08-488-379-152	Sequence 152, App
17	20	100.0	4	1 US-08-821-840-5	Sequence 5, Appli
18	20	100.0	4	1 US-08-713-528B-15	Sequence 15, Appl
19	20	100.0	4	1 US-08-407-900B-6	Sequence 6, Appli
20	20	100.0	4	1 US-08-419-075-28	Sequence 28, Appl
21	20	100.0	4	1 US-08-438-190A-17	Sequence 17, Appl
22	20	100.0	4	1 US-08-923-536A-2	Sequence 2, Appli
23	20	100.0	4	1 US-08-491-988-29	Sequence 29, Appl
24	20	100.0	4	1 US-08-665-202-29	Sequence 29, Appl
25	20	100.0	4	1 US-08-809-668-9	Sequence 9, Appli
26	20	100.0	4	1 US-08-331-397B-51	Sequence 51, Appl
27	20	100.0	4	1 US-08-759-804A-51	Sequence 51, Appl

Sequence 49, Appl
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Sequence 62, Appl
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6 1 US-08-406-192-37
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6 1 US-08-373-190-10
6 1 US-08-438-190A-13

ALIGNMENTS

RESULT 1
US-08-328-961-6
; Sequence 6, Application US/08328961
; Patent No. 5501975
; GENERAL INFORMATION:
; APPLICANT: Chaudhuri, Bhabatoeh
; APPLICANT: Stephan, Christine
; APPLICANT: Seeboth, Peter
; APPLICANT: Reizman, Howard
; TITLE OF INVENTION: No. 5501975e1 DNA Molecules and Hosts
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,961
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,260
; FILING DATE: 11-DSC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCES/DOCKET NUMBER: 4-18885/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 1..4
; OTHER INFORMATION: /note= "ER retention signal KDEL"
; US-08-328-961-6

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 2
US-07-872-673B-5
; Sequence 5, Application US/07872673B
; Patent No. 5578466
; GENERAL INFORMATION:
; APPLICANT: Toehiya HAYANO, Setsuko KATO, No. 5578466uhiro TAKAHASHI, and Masanori
; TITLE OF INVENTION: Co-expression System of Protein Disulfide Isomerase Gene an
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
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; COMPUTER: Apple Macintosh SE
; OPERATING SYSTEM: Apple DOS
; SOFTWARE: Microsoft Word Version 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,673B
; FILING DATE: 19920417
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Japanese Patent Application No. 5578466. 114074/91 and 311.
; FILING DATE: 18-APR-1991 and 30-OCT-1991
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE:

DESCRIPTION: peptide
FRAGMENT TYPE: C-terminal fragment
FEATURE:
NAME/KEY: ER retention signal
LOCATION: C-terminus
IDENTIFICATION METHOD: ER retention of proteins having this signal
OTHER INFORMATION: located at the C-terminus of rat PDI
PUBLICATION INFORMATION:
AUTHORS: Edman, Jeffrey C., Ellis, Leland, Blacher, Russell W., Roth, Richa
TITLE: Sequence of protein disulphide isomerase and implications of its rel
Patent No. 5578466
JOURNAL: Nature
VOLUME: 317
PAGES: 267-270
DATE: 19-Sep-1985
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 486 to 489
US-07-872-673B-5

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 3
US-08-405-615-16
; Sequence 16, Application US/08405615
; Patent No. 5602095
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Fitzgerald, David J.
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
; TITLE OF INVENTION: Increased Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ellen L. Weber
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,615
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-405-615-16

Query Match 100.0%; Score 20; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 4
US-08-331-398A-51
; Sequence 51, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-1261100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-398A-51

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 5
US-08-462-397-6
; Sequence 6, Application US/08462397
; Patent No. 5618690
; GENERAL INFORMATION:

Mon Mar 20 08:51:26 2006

us-09-673-707-9.ra1

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; APPLICANT: Chaudhuri, Bhabatosh
; APPLICANT: Stephan, Christine
; APPLICANT: Seebach, Peter
; APPLICANT: Reizman, Howard
; TITLE OF INVENTION: No. 5618690e1 DNA Molecules and Hosts
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,397
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,260
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-18885/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 1..4
; OTHER INFORMATION: /note= "ER retention signal KDEL"
;
US-08-462-397-6
Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 6
US-08-270-314-3
; Sequence 3, Application US/08270314
; Patent No. 5683888
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, Anthony K.
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: US
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/270,314
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89 16806.6
; FILING DATE: 22-JUL-1989
; APPLICATION NUMBER: PCT/GB90/01131
; FILING DATE: 23-JUL-1990
; APPLICATION NUMBER: US 07/820,867
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
;
US-08-270-314-3
Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 7
US-08-406-192-28
; Sequence 28, Application US/08406192
; Patent No. 5739287
; GENERAL INFORMATION:
; APPLICANT: Wilbur, D. Scott
; APPLICANT: Prathare, Pradip M
; TITLE OF INVENTION: Biotinylated Cobalamins
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101-2333
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,192
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,831
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Renzoni, George E.
; REGISTRATION NUMBER: 37,919
; REFERENCE/DOCKET NUMBER: RECL18947
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 28:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-192-28

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 8

US-08-082-269D-7
; Sequence 7, Application US/08082269D
; Patent No. 5773227
; GENERAL INFORMATION:
; APPLICANT: Kuhn, Michael
; APPLICANT: Meyer, Tobias
; APPLICANT: Allbritton, Nancy
; TITLE OF INVENTION: Bifunctional Chelating Polysaccharides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Molecular Probes, Inc.
; STREET: 4849 Pitchford Avenue
; CITY: Eugene
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97402-9144

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS 6.2
SOFTWARE: Text Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,269D
FILING DATE: 23-June-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Helfenstein, Allegra J.
REGISTRATION NUMBER: 34,179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503)465-8300
TELEFAX: (503)344-6504
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 AMINO ACIDS
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: no
FRAGMENT TYPE:
PUBLICATION INFORMATION:

AUTHORS: Munro, Sean and Pelham Hugh, R.B.
TITLE: A C-Terminal Signal Prevents Secretion of Luminal ER Proteins
JOURNAL: Cell
VOLUME: 48
ISSUE: 13 March 1987
PAGES: 899-907
DATE: 1987
US-08-082-269D-7

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

Db 1 KDEL 4

RESULT 9

US-08-593-865-1
; Sequence 1, Application US/08593865
; Patent No. 5776772
; GENERAL INFORMATION:

APPLICANT: Paulson, James C.
APPLICANT: Ujita-Lee, Eryn
APPLICANT: Colley, Karen J.
APPLICANT: Adler, Beverly
APPLICANT: Browne, Jeffrey K.
APPLICANT: Weinstein, Jasminder
TITLE OF INVENTION: Method for Producing Secrettable
TITLE OF INVENTION: Glycosyltransferases and Other Golgi Processing Enzymes
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, 38th Floor
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/593,865
FILING DATE: January 30, 1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 91/06635
FILING DATE: 16 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 117-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310)788-5000
TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-593-865-1

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 10

US-08-461-234-16
; Sequence 16, Application US/08461234
; Patent No. 5821238
; GENERAL INFORMATION:

APPLICANT: Pastan, Ira H.
APPLICANT: Fitzgerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower

Mon Mar 20 08:51:26 2006

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; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,234
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,709
; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,615
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-461-234-16

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 11
US-08-480-190-152
; Sequence 152, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:

; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,234
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,709
; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,615
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-461-234-16

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 12
US-08-545-151-28
; Sequence 28, Application US/08545151
; Patent No. 5840712
; GENERAL INFORMATION:
; APPLICANT: Morgan Jr, A. Charles
; APPLICANT: Wilbur, D. Scott
; APPLICANT: Prathare, Pradip M
; TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor
; TITLE OF INVENTION: Modulating Agents and Methods Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson & Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101-2333
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,151
; FILING DATE: 19-OCT-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04404
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: US 08/406,192
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/406,194
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/406,191
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/224,831
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Renzoni, George E
; REGISTRATION NUMBER: 37,919
; REFERENCE/DOCKET NUMBER: RECL18878

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-545-151-28

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 13

US-08-373-190-17
Sequence 17, Application US/08373190
Patent No. 5851829
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,190
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06735
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41956-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: STRE UR 2002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-373-190-17

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDEL 4
Db 1 KDEL 4

RESULT 14

US-08-463-480-16
Sequence 16, Application US/08463480
Patent No. 5854044
GENERAL INFORMATION:
APPLICANT: PASTAN, IRA H.
APPLICANT: FITZGERALD, DAVID J.
TITLE OF INVENTION: RECOMBINANT PSEUDOMONAS EXOTOXIN WITH
TITLE OF INVENTION: INCREASED ACTIVITY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
STREET: TWO EMBARCADERO CENTER, EIGHTH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,480
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,709
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: WEBER, ELLEN LAUVER
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-463-480-16

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 15

US-08-470-566B-51
Sequence 51, Application US/08470566B
Patent No. 5872212
GENERAL INFORMATION:
APPLICANT: WARREN, GREGORY W
APPLICANT: KOZIEL, MICHAEL G
APPLICANT: MULLINS, MARTHA A

Mon Mar 20 08:51:26 2006

us-09-673-707-9.ra1

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; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5872212artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,566B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC169S/CIP3/DIV4 - SOLv4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-470-566B-51

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4
|||||

RESULT 16
US-08-488-379-152
; Sequence 152, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger

```

```

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-152

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4
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RESULT 17
US-08-821-840-5
; Sequence 5, Application US/08821840
; Patent No. 5919456
; GENERAL INFORMATION:
; APPLICANT: Puri, Raj K.
; APPLICANT: Debinski, Waldemar
; APPLICANT: Pastan, Ira
; APPLICANT: Obiri, Nicholas
; TITLE OF INVENTION: IL-13 Receptor Specific Chimeric
; TITLE OF INVENTION: Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/821,840
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,685
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-217100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-821-840-5

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 18
US-08-713-928B-15
; Sequence 15, Application US/08713928B
; Patent No. 5929304
; GENERAL INFORMATION:
; APPLICANT: RADIN, DAVID N.
; APPLICANT: CRAMER, CAROLE L.
; APPLICANT: OISHI, KAREN K.
; APPLICANT: WEISSENBORN, DEBORAH L.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,928B
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,737
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7956-0011-999
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-713-928B-15

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 19
US-08-407-900B-6
; Sequence 6, Application US/08407900B
; Patent No. 5935822
; GENERAL INFORMATION:
; APPLICANT: Staehlin, Andrew
; APPLICANT: Galbraith, David
; APPLICANT: Giddings, Thomas
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR MEMBRANE AND
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,900B
; FILING DATE: 03-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-12
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-407-900B-6

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 20
US-08-419-075-28
; Sequence 28, Application US/08419075
; Patent No. 5939599
; GENERAL INFORMATION:
; APPLICANT: Saverio C. Falco

```

; APPLICANT: Chok-Fun Chui
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: A High Sulfur Seed
; TITLE OF INVENTION: Protein Gene and
; TITLE OF INVENTION: Method for Increasing
; TITLE OF INVENTION: the Sulfur Amino Acid
; TITLE OF INVENTION: Content of Plants
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,1.0MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,075
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,371
; FILING DATE:
; APPLICATION NUMBER: 07/656,687
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1027-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-419-075-28

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 21
US-08-438-190A-17
; Sequence 17, Application US/08438190A
; Patent No. 5965371
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109

; APPLICANT: Chok-Fun Chui
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: A High Sulfur Seed
; TITLE OF INVENTION: Protein Gene and
; TITLE OF INVENTION: Method for Increasing
; TITLE OF INVENTION: the Sulfur Amino Acid
; TITLE OF INVENTION: Content of Plants
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,1.0MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,075
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,371
; FILING DATE:
; APPLICATION NUMBER: 07/656,687
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1027-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-419-075-28

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 22
US-08-923-536A-2
; Sequence 2, Application US/08923536A
; Patent No. 5965426
; GENERAL INFORMATION:
; APPLICANT: SAKAI, Yasuyoshi
; APPLICANT: KATO, No. 5965426uo
; APPLICANT: SHIBANO, Yuji
; TITLE OF INVENTION: PROTEIN DISULFIDE ISOMERASE GENE DERIVED
; TITLE OF INVENTION: FROM STRAIN OF METHYLOTROPIC YEAST
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,536A
; FILING DATE: 04-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-234287
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 001560-317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-923-536A-2

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 23

US-08-491-988-29
; Sequence 29, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMEMNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,988
; FILING DATE: 18-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-491-988-29

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 24

US-08-665-202-29
; Sequence 29, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert

; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-29

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 25

US-08-809-668-9
; Sequence 9, Application US/08809668
; Patent No. 5980895
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kuan, Chien-Tsun

; TITLE OF INVENTION: Immunotoxin Containing a
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 5980895 Require Proteolytic
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Mon Mar 20 08:51:26 2006

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,668
; FILING DATE: 21-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,388
; FILING DATE: 13-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16327
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-253100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-809-668-9

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 26
US-08-331-397B-51
; Sequence 51, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US

US-08-759-804A-51
; Sequence 51, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

US-08-759-804A-51

Query Match 100.0%; Score 20; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 28

US-08-818-253-49

; Sequence 49, Application US/08818253
 ; Patent No. 5998204
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsien, Roger Y.
 ; APPLICANT: Miyawaki, Atsushi
 ; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 ; DETECTION OF ANALYTES
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,253
 FILING DATE: 14-MAR-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07257/043001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-818-253-49

Query Match 100.0%; Score 20; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 29

US-08-350-215-17

; Sequence 17, Application US/08350215
 ; Patent No. 6004940
 ; GENERAL INFORMATION:
 ; APPLICANT: MARASCO, WAYNE A.
 ; APPLICANT: RICHARDSON, JENNIFER
 ; TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
 ; PROTEINS
 ; NUMBER OF SEQUENCES: 58

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/722,258
 FILING DATE: 08-JAN-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US95/04468
 FILING DATE: 06-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/225,224

US-08-818-253-49

Query Match 100.0%; Score 20; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 1 KDEL 4

RESULT 30

US-08-722-258-62

; Sequence 62, Application US/08722258
 ; Patent No. 6011002
 ; GENERAL INFORMATION:
 ; APPLICANT: Pastan, Ira
 ; APPLICANT: Kreitman, Robert J.
 ; APPLICANT: Puri, Raj K.
 ; TITLE OF INVENTION: Circularly Permuted Ligands and
 ; Circularly Permuted Chimeric Molecules
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/722,258
 FILING DATE: 08-JAN-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US95/04468
 FILING DATE: 06-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/225,224

US-08-722-258-62

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ADDRESSEE: CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: US
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/350,215
 FILING DATE: 12-DEC-1994
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: EISENSTEIN, RONALD I.
 REGISTRATION NUMBER: 30628
 REFERENCE/DOCKET NUMBER: 41956-CP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-3400
 TELEFAX: (617) 523-6440
 TELEX: 200291 STRE UR
 INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-350-215-17

Query Match 100.0%; Score 20; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4

Db 1 KDEL 4

RESULT 30

US-08-722-258-62

; Sequence 62, Application US/08722258
 ; Patent No. 6011002
 ; GENERAL INFORMATION:
 ; APPLICANT: Pastan, Ira
 ; APPLICANT: Kreitman, Robert J.
 ; APPLICANT: Puri, Raj K.
 ; TITLE OF INVENTION: Circularly Permuted Ligands and
 ; Circularly Permuted Chimeric Molecules
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/722,258
 FILING DATE: 08-JAN-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US95/04468
 FILING DATE: 06-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/225,224

US-08-722-258-62

```
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-193100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-722-258-62

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 31
US-08-718-904-42
; Sequence 42, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037329tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: /note="Cytoplasmic Translocation"
; US-08-718-904-42

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 32
US-08-782-480-44
; Sequence 44, Application US/08782480
; Patent No. 6045774
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Hein, Mich B.
; APPLICANT: Fitchen, John H.
; TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE IMAGING AGENT
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,480
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 310098.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-782-480-44

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 33
US-09-287-145A-17
; Sequence 17, Application US/09287145A
; Patent No. 6072036
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESS: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
```

```
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/287,145A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,190
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-287-145A-17

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 34
US-09-397-951-9
; Sequence 9, Application US/09397951
; Patent No. 6074644
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; TITLE OF INVENTION: Immunotoxin Containing a
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 6074644 Require Proteolytic
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/397,951
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,668
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16327
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
```

```
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-253100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-397-951-9

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 35
US-08-776-271-7
; Sequence 7, Application US/08776271
; Patent No. 6083502
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,271
; FILING DATE: 01-DEC-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-259100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-776-271-7

Query Match 100.0%; Score 20; DB 2; Length 4;
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; CURRENT FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-094-359-17

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 36
US-09-047-148-12
; Sequence 12, Application US/09047148
; Patent No. 6086900
; GENERAL INFORMATION:
; APPLICANT: Draper, Rockford
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; TITLE OF INVENTION: CELL MEMBRANES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,148
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,056
; FILING DATE: 26-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSP:072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-047-148-12

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 37
US-09-094-359-17
; Sequence 17, Application US/09094359
; Patent No. 6140132
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/067001
; CURRENT APPLICATION NUMBER: US/09/094,359

; CURRENT FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-063-37

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 38
US-09-172-063-37
; Sequence 37, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
; APPLICANT: Wachter, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 09/094,359
; EARLIER FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-063-37

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 39
US-08-789-333F-28
; Sequence 28, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A642601DJBRMSOSS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
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```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum sequence.
US-08-789-333F-28

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 40
US-09-215-035-7
; Sequence 7, Application US/09215035
; Patent No. 6153430
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,035
; FILING DATE: No. 6153430 yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/776,271
; FILING DATE: 01-DEC-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-259110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-215-035-7

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

US-09-169-015-38
; Sequence 38, Application US/09169015
; Patent No. 6180343
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
; FILE REFERENCE: A66900/DJB/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/169,015
; CURRENT FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transaction B
; PAGES: 1-10
US-09-169-015-38

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

US-09-169-425C-23
; Sequence 23, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Urban, Robert G.
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Db      1 KDEL 4

RESULT 41
US-09-124-671-37
; Sequence 37, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recognition sequence of KDEL receptor
US-09-124-671-37

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 42
US-09-169-015-38
; Sequence 38, Application US/09169015
; Patent No. 6180343
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
; FILE REFERENCE: A66900/DJB/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/169,015
; CURRENT FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transaction B
; PAGES: 1-10
US-09-169-015-38

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 43
US-09-169-425C-23
; Sequence 23, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Urban, Robert G.
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; APPLICANT: Chicx, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-169-425C-23

Query Match 100.0%; Score 20; DB 2; Length 4;
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Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 44
US-09-191-852-1
; Sequence 1, Application US/09191852
; Patent No. 6194560
; GENERAL INFORMATION:
; APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
; TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/191,852
; FILING DATE:
; CLASSIFICATION:

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Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 45
US-08-818-252-49
; Sequence 49, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-818-252-49

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 46
US-08-957-001B-2
; Sequence 2, Application US/08957001B
; Patent No. 6228621
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Madaio, Michael
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: IMPROVED VACCINES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13376
; FILING DATE: 24-OCT-1995
; APPLICATION NUMBER: 08/817,906
; FILING DATE: 04-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, David L.
; REGISTRATION NUMBER: 40,612
; REFERENCE/DOCKET NUMBER: P01590US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-651-5151
; TELEFAX: 713-651-5246
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-191-852-1

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4
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; ZIP: 19103
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; OPERATING SYSTEM: windows
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,001B
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,592
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-3303
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; US-08-957-001B-2

Query Match 100.0%; Score 20; DB 2; Length 4;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 47
US-09-496-301-2
; Sequence 2, Application US/09496301
; Patent No. 6248565
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Madaio, Michael
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: IMPROVED VACCINES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: windows
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/496,301
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/957,001
; FILING DATE: 23-OCT-1997
; APPLICATION NUMBER: US 60/029,592
; FILING DATE: 23-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark

; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-3303
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; US-09-496-301-2

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 48
US-08-954-211-44
; Sequence 44, Application US/08954211
; Patent No. 6251392
; GENERAL INFORMATION:
; APPLICANT: Hein, Mich B.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Fitcher, John H.
; TITLE OF INVENTION: NOVEL EPITHELIAL CELL TARGETING AGENT
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,211
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 310098.403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-954-211-44

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 49

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Job time : 20.5 secs

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; Patent No. 6280937
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/133,944
; CURRENT FILING DATE: 1999-08-14
; EARLIER APPLICATION NUMBER: 09/133,949
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: endoplasmic
; OTHER INFORMATION: reticulum sequence
; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
US-09-133-944-27

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 50
US-09-613-182-12
; Sequence 12, Application US/09613182
; Patent No. 6294653
; GENERAL INFORMATION:
; APPLICANT: Mayfield, Stephen
; TITLE OF INVENTION: RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES
; FILE REFERENCE: SCR2177S
; CURRENT APPLICATION NUMBER: US/09/613,182
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/341,550
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: PCT/US98/00840
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/035,955
; PRIOR FILING DATE: 1997-01-17
; PRIOR APPLICATION NUMBER: 60/069,400
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-09-613-182-12

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 KDEL 4
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GenCore version 5.1.7
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Perfect score: 20
Sequence: 1 KDEL 4

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:
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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	4	3	US-09-749-959-37
5	20	100.0	4	3	US-09-759-960-23
6	20	100.0	4	3	US-09-789-652A-25
7	20	100.0	4	3	US-09-208-827-29
8	20	100.0	4	3	US-09-854-122-2
9	20	100.0	4	3	US-09-881-165-5
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					Sequence 3, Appl
					Sequence 22, Appl
					Sequence 10, Appl
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					Sequence 6, Appl

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Sequence 97, Appl
Sequence 24, Appl
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Sequence 19, Appl
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Sequence 46, Appl

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103	20	100.0	4	4	US-10-114-663-5	Sequence 5, Appl
104	20	100.0	4	4	US-10-297-337-17	Sequence 17, Appl
105	20	100.0	4	4	US-10-371-877-6	Sequence 6, Appl
106	20	100.0	4	4	US-10-058-270A-141	Sequence 141, Appl
107	20	100.0	4	4	US-10-607-037-2	Sequence 2, Appl
108	20	100.0	4	4	US-10-258-147-1	Sequence 1, Appl
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114	20	100.0	4	4	US-10-406-830-26	Sequence 26, Appl
115	20	100.0	4	4	US-10-380-136-11	Sequence 11, Appl
116	20	100.0	4	4	US-10-716-062-2	Sequence 2, Appl
117	20	100.0	4	4	US-10-335-774-22	Sequence 22, Appl
118	20	100.0	4	4	US-10-363-233-6	Sequence 6, Appl
119	20	100.0	4	4	US-10-343-251A-40	Sequence 40, Appl
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126	20	100.0	4	4	US-10-789-450-20	Sequence 20, Appl
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134	20	100.0	4	5	US-10-933-855-42	Sequence 42, Appl
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136	20	100.0	4	5	US-10-934-614-28	Sequence 28, Appl
137	20	100.0	4	5	US-10-869-040-150	Sequence 150, App
138	20	100.0	4	5	US-10-433-245A-2	Sequence 2, Appl
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144	20	100.0	4	5	US-10-659-036-13	Sequence 13, Appl
145	20	100.0	4	5	US-10-873-594-37	Sequence 37, Appl
146	20	100.0	4	5	US-10-831-901A-8	Sequence 8, Appl
147	20	100.0	4	5	US-10-751-845-111	Sequence 111, App
148	20	100.0	4	5	US-10-499-184-26	Sequence 26, Appl
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150	20	100.0	4	5	US-10-700-971C-18	Sequence 18, Appl
ALIGNMENTS						
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US-08-765-244-16						
; Sequence 16, Application US/08765244						
; Publication No. US20010008771A1						
; GENERAL INFORMATION:						
; APPLICANT: Seibel, Peter						
; APPLICANT: Seibel, Andrea						
; TITLE OF INVENTION: CHIMERICAL PEPTIDE-NUCLEIC ACID						
; TITLE OF INVENTION: FRAGMENT, PROCESS FOR PRODUCING THE SAME AND ITS USES FOR						
; TITLE OF INVENTION: APPROPRIATELY INTRODUCING NUCLEIC ACIDS INTO CELL ORGANELLES						
; TITLE OF INVENTION: AND CELLS						
; FILE REFERENCE: 8484-0018-999						
; CURRENT APPLICATION NUMBER: US/08/765,244						
; CURRENT FILING DATE: 1997-10-30						
; PRIOR APPLICATION NUMBER: PCT/DE95/00775						
; PRIOR FILING DATE: 1995-06-11						
; PRIOR APPLICATION NUMBER: DE P 44 21 079.5						
; PRIOR FILING DATE: 1994-06-16						
; NUMBER OF SEQ ID NOS: 22						
; SOFTWARE: FastSeq for Windows Version 4.0						
; SEQ ID NO 16						
; LENGTH: 4						
; TYPE: PRT						
; ORGANISM: Artificial Sequence						
; FEATURE:						
; OTHER INFORMATION: Synthetic sequence						
US-08-765-244-16						
Query Match						100.0%; Score 20; DB 2; Length 4;
Best Local Similarity						100.0%; Pred. No. 1.7e+06;
Matches						4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	KDEL	4			
Db	1	KDEL	4			
RESULT 2						
US-08-873-601-24						
; Sequence 24, Application US/08873601						
; Publication No. US20020064798A1						
; GENERAL INFORMATION:						
; APPLICANT: Pavan, Donald						
; APPLICANT: No. US20020064798A1an, Garry P.						
; TITLE OF INVENTION: COMBINATORIAL ENZYMATIC COMPLEXES						
; FILE REFERENCE: A-63915/DJB/RMS						
; CURRENT APPLICATION NUMBER: US/08/873,601						
; CURRENT FILING DATE: 1997-06-12						
; NUMBER OF SEQ ID NOS: 35						
; SOFTWARE: PatentIn Ver. 2.0						
; SEQ ID NO 24						
; LENGTH: 4						
; TYPE: PRT						
; ORGANISM: Unknown						
; FEATURE:						
; OTHER INFORMATION: Description of Unknown Organism: UNKNOWN						
US-08-873-601-24						
Query Match						100.0%; Score 20; DB 2; Length 4;
Best Local Similarity						100.0%; Pred. No. 1.7e+06;
Matches						4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	KDEL	4			
Db	1	KDEL	4			
RESULT 3						
US-09-157-748-30						
; Sequence 30, Application US/09157748						
; Patent No. US20010003042A1						
; GENERAL INFORMATION:						
; APPLICANT: Lorens, James						
; TITLE OF INVENTION: Multiparameter FACS Assays to Detect Alterations in						
; TITLE OF INVENTION: Cell Cycle Regulation						
; FILE REFERENCE: A66587/DJB/RMS						
; CURRENT APPLICATION NUMBER: US/09/157,748						
; CURRENT FILING DATE: 1998-09-21						
; NUMBER OF SEQ ID NOS: 46						
; SOFTWARE: PatentIn Ver. 2.0						
; SEQ ID NO 30						
; LENGTH: 4						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
; PUBLICATION INFORMATION:						
; JOURNAL: Royal Society London Transaction B						
; PAGES: 1-1-						
; DATE: 1992						
US-09-157-748-30						
Query Match						100.0%; Score 20; DB 3; Length 4;

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 4
US-09-749-959-37
; Sequence 37, Application US/09749959
; Publication No. US20010003650A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: GREEN FLUORESCENT PROTEIN FUSIONS WITH RANDOM PEPTIDES
; FILE REFERENCE: A-66900-5/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/749,959
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-749-959-37

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 5
US-09-759-960-23
; Sequence 23, Application US/09759960
; Patent No. US20010006839A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:

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; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
; US-09-208-827-29

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 8
US-09-854-122-2
; Sequence 2, Application US/09854122
; Patent No. US20020016980A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTE, RANDALL S.
; TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTERA MARINA
; FILE REFERENCE: PHA-007.01
; CURRENT APPLICATION NUMBER: US/09/854,122
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/202,529
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-854-122-2

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 9
US-09-881-165-5
; Sequence 5, Application US/09881165
; Publication No. US20020039772A1
; GENERAL INFORMATION:
; APPLICANT: HOOD, ELIZABETH
; APPLICANT: HOWARD, JOHN
; APPLICANT: BAILEY, MICHELE
; APPLICANT: GASTEL, FRANS VAN
; APPLICANT: WANG, HUAMING
; APPLICANT: WARD, MICHAEL
; APPLICANT: WOODARD, SUSAN
; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
; FILE REFERENCE: 10032R
; CURRENT APPLICATION NUMBER: US/09/881,165
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/211,732
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
US-09-881-165-5

; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
; US-09-208-827-29

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 10
US-09-347-064-35
; Sequence 35, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
; APPLICANT: Eck, Jurgen
; APPLICANT: Schmidt, Arno
; APPLICANT: Zinke, Holger
; TITLE OF INVENTION: Recombinant Fusion Proteins Based on
; TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
; FILE REFERENCE: 09282-5
; CURRENT APPLICATION NUMBER: US/09/347,064A
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: PCT/EP98/00009
; EARLIER FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: EP 97 10 0012.0
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modulator
; OTHER INFORMATION: module peptide
US-09-347-064-35

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 11
US-09-910-639-2
; Sequence 2, Application US/09910639
; Publication No. US20020048550A1
; GENERAL INFORMATION:
; APPLICANT: Vallera, Daniel A.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: RADIOLABELED IMMUNOTOXINS
; FILE REFERENCE: 09531-023001
; CURRENT APPLICATION NUMBER: US/09/910,639
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/219,759
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-639-2

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Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 12

US-09-333-527-2
; Sequence 2, Application US/09333527
; Patent No. US20020078472A1
; GENERAL INFORMATION:
; APPLICANT: Paul CHRISTOU; Eva STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO; Stef
; TITLE OF INVENTION: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN POLYPEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,527
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/089,322
; FILING DATE: June 15, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: KL/JIC 202.1 - JEL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; TOPOLOGY: linear
US-09-333-527-2

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 13

US-09-785-921A-16
; Sequence 16, Application US/09785921A
; Patent No. US20020094344A1
; GENERAL INFORMATION:
; APPLICANT: Keener, William K.
; APPLICANT: Ward, Thomas E.
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: LIT-PI-529
; CURRENT APPLICATION NUMBER: US/09/785,921A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-921A-16

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 14

US-09-997-956-2
; Sequence 2, Application US/09997956
; Patent No. US20020106714A1
; GENERAL INFORMATION:
; APPLICANT: Jalink, Kees
; TITLE OF INVENTION: Membrane Molecule Indicator Compositions
; TITLE OF INVENTION: and Methods
; FILE REFERENCE: P-NS 5045
; CURRENT APPLICATION NUMBER: US/09/997,956
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/250,679
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/256,559
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-956-2

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 15

US-09-781-804-2
; Sequence 2, Application US/09781804
; Patent No. US20020107189A1
; GENERAL INFORMATION:
; APPLICANT: ARIAD Gene Therapeutics, Inc.
; TITLE OF INVENTION: Regulation of Biological Events Using No. US20020107189A1e1 Com
; FILE REFERENCE: 374 USD1
; CURRENT APPLICATION NUMBER: US/09/781,804
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: organelle binding domain
; NAME/KEY: DOMAIN
; LOCATION: (1)..(4)
; OTHER INFORMATION: organelle binding domain
US-09-781-804-2

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Mar 20 08:51:26 2006

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Qy      1 KDEL 4
Db      1 KDEL 4

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

RESULT 16
US-09-916-940-28
; Sequence 28, Application US/09916940
; Patent No. US20020127564A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020127564Alan, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64260-6/RMS/RMS
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1997-11-03
; PRIOR FILING DATE: 1996-01-23
; PRIOR FILING DATE: 1996-01-23
; PRIOR FILING DATE: 1996-01-23
; PRIOR FILING DATE: 1997-01-23
; PRIOR FILING DATE: 1997-01-23
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum sequence.
US-09-916-940-28

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 17
US-09-270-983-5
; Sequence 5, Application US/09270983
; Patent No. US20020132327A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: HAY, Bruce A.
; APPLICANT: HAWKINS, Christine V.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING PROTEASES, PROTEASE TARGET SITES AND REGULATORY
; TITLE OF INVENTION: OF PROTEASE ACTIVITY IN LIVING CELLS
; FILE REFERENCE: CIT1130-1
; CURRENT FILING DATE: 1999-03-17
; PRIOR FILING DATE: 1999-03-17
; PRIOR FILING DATE: 1998-03-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Product Synthesis, such as solid phase synthesis
US-09-270-983-5

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 18
US-09-917-154-1
; Sequence 1, Application US/09917154
; Publication No. US20020137707A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wolff, Jon A
; APPLICANT: Hagstrom, James E
; APPLICANT: Monahan, Sean D
; APPLICANT: Siattum, Paul M
; APPLICANT: Rozema, David B
; APPLICANT: Budker, Vladimir G
; TITLE OF INVENTION: Intravascular Delivery of Non-Viral Nucleic Acid
; FILE REFERENCE: Mirus.013.04.03
; CURRENT FILING DATE: 2001-07-27
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-917-154-1

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 19
US-09-480-236-8
; Sequence 8, Application US/09480236
; Patent No. US20020142000A1
; GENERAL INFORMATION:
; APPLICANT: Digan, Mary Ellen
; APPLICANT: Lake, Philip
; APPLICANT: Wright, Richard M.
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
; FILE REFERENCE: CGC 4-31157A/USN
; CURRENT FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PE peptide
US-09-480-236-8

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4
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RESULT 20
US-09-984-183-3
; Sequence 3, Application US/09984183
; Patent No. US20020142983A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: MUC-1 ANTAGONISTS AND METHODS OF TREATING IMMUNE
; DISORDERS
; FILE REFERENCE: 042881/0130
; CURRENT APPLICATION NUMBER: US/09/984,183
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/457,354
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/111,973
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Retrograde
; transport peptide
US-09-984-183-3

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 21
US-09-999-745-22
; Sequence 22, Application US/09999745
; Patent No. US20020157120A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGEN1470-1
; CURRENT APPLICATION NUMBER: US/09/999,745
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/316,920
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-999-745-22

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 22
US-09-967-772-10
; Sequence 10, Application US/09967772
; Patent No. US20020164577A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Martin
; APPLICANT: Gonzalez, Ana Maria
; APPLICANT: Baird, Andrew
; GENERAL INFORMATION:
; Patent No. US20020168338A1
; Sequence 19, Application US/09178286
US-09-178-286-19

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 23
US-09-554-000-49
; Sequence 49, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-554-000-49

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 24
US-09-178-286-19
; Sequence 19, Application US/09178286
; Patent No. US20020168338A1
; GENERAL INFORMATION:
; APPLICANT: Baird, Andrew
; APPLICANT: Gonzalez, Ana Maria
; APPLICANT: Berry, Martin
; GENERAL INFORMATION:
; Patent No. US20020168338A1
; Sequence 19, Application US/09178286
US-09-178-286-19

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSJEN, Roger
; APPLICANT: GONZALEZ, Jesus
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
; FILE REFERENCE: REGEN1290-5
; CURRENT APPLICATION NUMBER: US/09/967,772
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 08/765,860
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: PCT/ US96/09652
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/481,977
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Protein localization sequence
US-09-967-772-10

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4
```

Mon Mar 20 08:51:26 2006

```

; APPLICANT: Logan, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; FILE OF INVENTION: AGENTS FOR NEURONAL REGENERATION AND SURVIVAL
; FILE REFERENCE: 760100.433C1
; CURRENT APPLICATION NUMBER: US/09/178,286
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide - example
; OTHER INFORMATION: cytoplasm-translocation signal sequence
US-09-178-286-19

Query Match          100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
        ||||
Db      1 KDEL 4

RESULT 25
US-09-792-630-77
; Sequence 77, Application US/09792630
; Patent No. US20020168640A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
; FILE REFERENCE: A-70295/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/792,630
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-630-77

Query Match          100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
        ||||
Db      1 KDEL 4

RESULT 26
US-09-915-789A-10
; Sequence 10, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Rattus norvegicus

```

; LENGTH: 4
; TYPE: PRT
; ORGANISM: eukaryotic
US-09-925-803-3

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 29

US-09-575-847-8
; Sequence 8, Application US/09575847
; Publication No. US20030013149A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: WACHTER, Rebekka
; APPLICANT: REMINGTON, James
; TITLE OF INVENTION: LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS
; FILE REFERENCE: REG1250-5
; CURRENT APPLICATION NUMBER: US/09/575,847
; CURRENT FILING DATE: 2000-05-19
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: US 08/974,737
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: US 08/911,825
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: US 08/706,408
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Targeting sequence
US-09-575-847-8

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 30

US-09-935-430-699
; Sequence 699, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-BID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 699

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-699

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 31

US-09-991-209-97
; Sequence 97, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/249,608
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: retention sequence
US-09-991-209-97

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 32

US-09-999-686-24
; Sequence 24, Application US/09999686
; Publication No. US20030028000A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nazneen
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Tomlinson, Andrew J.
; APPLICANT: Cole, Geoffrey
; TITLE OF INVENTION: CYP1B1 NUCLEIC ACIDS AND METHODS OF USE
; FILE REFERENCE: 08191-021001
; CURRENT APPLICATION NUMBER: US/09/999,686
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/298,428
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/261,719
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/244,501

```
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-999-686-24

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 33
US-09-906-393A-1
; Sequence 1, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906.393A
; PRIORITY FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-906-393A-1

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 34
US-09-861-257-19
; Sequence 19, Application US/09861257
; Publication No. US20030040496A1
; GENERAL INFORMATION:
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; APPLICANT: Baird, J. Andrew
; APPLICANT: Pierce, Glenn
; TITLE OF INVENTION: TREATMENT OF TUMORS USING
; TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/861,257
; FILING DATE: 17-MAY-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen Ph.D., William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 760100.423C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: /note= "Cytoplasmic Translocation
; OTHER INFORMATION: Signal"
US-09-861-257-19

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 35
US-09-913-238-63
; Sequence 63, Application US/09913238
; Publication No. US20030049251A1
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Steinberger, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
; TITLE OF INVENTION: INHIBITING CCR5-DEPENDENT INFECTION OF CELLS BY HIV-1
; FILE REFERENCE: TSRI 728.1
; CURRENT APPLICATION NUMBER: US/09/913,238
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: PCT/EPO 0/12419
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,653
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: RastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthesized
US-09-913-238-63

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 36
US-09-462-713-13
; Sequence 13, Application US/09462713
; Publication No. US20030054012A1
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: Mreny, Randall J.
; APPLICANT: The Government of the United States of America
```

; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
; FILE REFERENCE: 015280-361100US
; CURRENT APPLICATION NUMBER: US/09/462,713
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-09-462-713-13

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 37

US-09-932-165-1508
; Sequence 1508, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1508
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-09-932-165-1508

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 38

US-09-942-052-708

; Sequence 708, Application US/09942052

US-09-935-384-781
; Sequence 781, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 781
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-384-781

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 39

US-09-824-200-9
; Sequence 9, Application US/09824200
; Publication No. US20030167531A1
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, DOUGLAS A.
; APPLICANT: SCHLITTLER, MICHAEL
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF BIOACTIVE, AUTHENTIC
; TITLE OF INVENTION: POLYPEPTIDES FROM PLANTS
; FILE REFERENCE: 16712.0031
; CURRENT APPLICATION NUMBER: US/09/824,200
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,217
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-200-9

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 40

US-09-942-052-708
; Sequence 708, Application US/09942052

Publication No. US20030170626A1
GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 708
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Illustrative
OTHER INFORMATION: peptide
US-09-942-052-708

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 41
US-09-293-670-34
Sequence 34, Application US/09293670
Publication No. US20030190684A1
GENERAL INFORMATION:
APPLICANT: Fisher, Joseph
APPLICANT: Lorens, James
APPLICANT: Payan, Donald
APPLICANT: Rossi, Alexander
TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in
TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule
TITLE OF INVENTION: Libraries
FILE REFERENCE: A68104/DJB/RMS/DAV
CURRENT APPLICATION NUMBER: US/09/293,670
CURRENT FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
PUBLICATION INFORMATION:
JOURNAL: Royal Society London Transaction B
PAGES: 1-10
DATE: 19992
US-09-293-670-34

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 42
US-09-872-836-116
Sequence 116, Application US/09872836
Publication No. US20040142475A1
GENERAL INFORMATION:
APPLICANT: Barman, Shikha P.
APPLICANT: McKeever, Una
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 08191-018001
CURRENT APPLICATION NUMBER: US/09/872,836
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,830
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 116
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-09-872-836-116

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 43
US-09-800-770-81
Sequence 81, Application US/09800770
Publication No. US2005023456A1
GENERAL INFORMATION:
APPLICANT: Kinsella, Todd
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES
FILE REFERENCE: A-68614-1/DJB/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/800,770
CURRENT FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: US 60/187,130
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn version 3.1
SEQ ID NO 81
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-770-81

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 44
US-10-043-142-9
Sequence 9, Application US/10043142
Publication No. US20020150969A1
GENERAL INFORMATION:
APPLICANT: DEXX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 2002-03-30

; PRIOR APPLICATION NUMBER: PCT/IB99/01669
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: GB 9821198.0
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative ER
; OTHER INFORMATION: retention
; OTHER INFORMATION: signal
US-10-043-142-9

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KDEL 4

RESULT 45
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; Sequence 3, Application US/10154801
; Publication No. US200201510141
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, ANTHONY KEITH
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
; FILE REFERENCE: 09/225,302
; CURRENT APPLICATION NUMBER: US/10/154,801
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 08/957,135
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-154-801-3

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RESULT 46
US-10-080-376-77
; Sequence 77, Application US/10080376
; Publication No. US20020172968A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; APPLICANT: Dahiya, Basil I.
; TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
; FILE REFERENCE: A-70295-2/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/080,376
; CURRENT FILING DATE: 2000-02-19
; PRIOR APPLICATION NUMBER: US 09/792,630
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-376-77

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RESULT 47
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; Publication No. US20020192675A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: US/10/061,395
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Endoplasmic reticulum sequence from calreticulin
US-10-061-395-25

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Db 1 KDEL 4

RESULT 48
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; Sequence 35, Application US/10061395
; Publication No. US20020192675A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: US/10/061,395
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Heterologous signal sequence for the endoplasmic reticulum
US-10-061-395-35

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RESULT 49
US-10-043-074-29
; Sequence 29, Application US/10043074
; Publication No. US20030017601A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252-1/DJB/DAV
; CURRENT APPLICATION NUMBER: US/10/043,074
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,827
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/133,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 43
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; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: endoplasmic
; OTHER INFORMATION: reticulum sequence
; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
US-10-043-074-29

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-096-339-24

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Db 1 KDEL 4

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US-10-096-339-24
; Sequence 24, Application US/10096339
; Publication No. US20030022196A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Kinseella, Todd
; APPLICANT: Masuda, Esteban
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Liao, X. Charlene
; APPLICANT: Pearsall, Denise
; APPLICANT: Freira, Annabelle
; APPLICANT: Chu, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ALTERED CELLULAR PHENO
; FILE REFERENCE: A-71158/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/096,339
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/076,624
; PRIOR FILING DATE: 1998-05-12

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Db 1 KDEL 4

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; Sequence 24, Application US/10096339
; Publication No. US20030022196A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Kinseella, Todd
; APPLICANT: Masuda, Esteban
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Liao, X. Charlene
; APPLICANT: Pearsall, Denise
; APPLICANT: Freira, Annabelle
; APPLICANT: Chu, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ALTERED CELLULAR PHENO
; FILE REFERENCE: A-71158/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/096,339
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/076,624
; PRIOR FILING DATE: 1998-05-12

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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:53:30 ; Search time 8.5 Seconds
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Minimum DB seq length: 0
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	4	6	US-10-989-767A-699
5	20	100.0	4	6	US-10-757-832-52
6	20	100.0	4	6	US-10-909-957-10
7	20	100.0	4	6	US-10-962-951-4
8	20	100.0	4	6	US-10-537-061-11
9	20	100.0	4	7	US-11-042-988-14
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16	20	100.0	4	7	US-11-102-883-42
17	20	100.0	4	7	US-11-214-613-97
18	20	100.0	4	7	US-11-029-188-16
19	20	100.0	4	7	US-11-141-725-47
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23	20	100.0	4	7	US-11-108-088-70
24	20	100.0	4	7	US-11-255-677-17
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28	20	100.0	6	7	US-11-019-027-58	Sequence 58, Appl
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32	20	100.0	7	7	US-11-042-988-16	Sequence 16, Appl
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38	20	100.0	18	7	US-11-206-138-2	Sequence 2, Appli
39	20	100.0	28	7	US-11-193-654-18	Sequence 18, Appl
40	20	100.0	38	7	US-11-096-568A-9747	Sequence 9747, Ap
41	20	100.0	55	7	US-11-245-400-34	Sequence 34, Appl
42	20	100.0	59	7	US-11-174-413-38	Sequence 38, Appl
43	20	100.0	63	7	US-11-195-459-6	Sequence 6, Appli
44	20	100.0	69	6	US-10-467-657-414	Sequence 414, App
45	20	100.0	69	7	US-11-022-562-224	Sequence 224, App
46	20	100.0	80	6	US-10-986-501-200	Sequence 200, App
47	20	100.0	99	6	US-10-517-696-99	Sequence 99, Appl
48	20	100.0	103	6	US-10-986-501-125	Sequence 125, App
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56	20	100.0	126	7	US-11-096-568A-9746	Sequence 9746, Ap
57	20	100.0	128	6	US-10-467-657-5274	Sequence 5274, Ap
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65	20	100.0	142	7	US-11-096-568A-26333	Sequence 26333, A
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74	20	100.0	163	6	US-10-467-657-2662	Sequence 2662, Ap
75	20	100.0	164	7	US-11-096-568A-24430	Sequence 24430, A
76	20	100.0	171	6	US-10-506-796A-9	Sequence 9, Appli
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92	20	100.0	191	7	US-11-096-568A-11707	Sequence 11707, A
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94	20	100.0	192	6	US-10-821-234-1651	Sequence 1651, Ap
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96	20	100.0	197	7	US-11-185-342-6	Sequence 6, Appli
97	20	100.0	199	7	US-11-087-099-9661	Sequence 9661, Ap
98	20	100.0	199	7	US-11-096-568A-2237	Sequence 2237, Ap

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128 20 100.0 233 7 US-11-072-512-3056
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136 20 100.0 248 7 US-11-096-568A-12320
137 20 100.0 249 7 US-11-096-568A-26331
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151 20 100.0 254 7 US-11-067-323-22

ALIGNMENTS

RESULT 1
US-10-444-662-3
; Sequence 3, Application US/10444662
; Publication No. US20050250683A9
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Rozema, David
; APPLICANT: Wolff, Jon
; APPLICANT: Wakefield, Darren
; APPLICANT: Ekena, Kirk
; APPLICANT: Hagstrom, James
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction
; FILE REFERENCE: Mirus.035.01
; CURRENT APPLICATION NUMBER: US/10/444,662
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 8

Sequence 5337, Ap
Sequence 3655, Ap
Sequence 5336, Ap
Sequence 4223, Ap
Sequence 10657, A
Sequence 126, App
Sequence 2210, Ap
Sequence 30079, A
Sequence 29876, A
Sequence 381, App
Sequence 383, App
Sequence 29878, A
Sequence 100, App
Sequence 10926, A
Sequence 7214, Ap
Sequence 16266, A
Sequence 4273, Ap
Sequence 29875, A
Sequence 14890, A
Sequence 29874, A
Sequence 8, Appli
Sequence 10973, A
Sequence 25462, A
Sequence 504, App
Sequence 656, App
Sequence 658, App
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Sequence 662, App
Sequence 431, App
Sequence 3056, Ap
Sequence 36, Appl
Sequence 10275, A
Sequence 16265, A
Sequence 4893, Ap
Sequence 4022, Ap
Sequence 6753, Ap
Sequence 9422, Ap
Sequence 12320, A
Sequence 26331, A
Sequence 5335, Ap
Sequence 10274, A
Sequence 18, Appl
Sequence 28, Appl
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-662-3

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
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Db 1 KDEL 4

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; Sequence 262, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target sequence
US-10-667-295-262

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KDEL 4

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US-10-475-204-23
; Sequence 23, Application US/10475204
; Publication No. US20050277116A1
; GENERAL INFORMATION:
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION OF
; FILE REFERENCE: HMV-056.25
; CURRENT APPLICATION NUMBER: US/10/475,204
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/US02/13008
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/285,509
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Calreticulin
; OTHER INFORMATION: targeting sequence
US-10-475-204-23

```

```
Query Match      100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 4
US-10-989-767A-699
; Sequence 699, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-BID, PIA
; TITLE OF INVENTION: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 511582005004
; CURRENT APPLICATION NUMBER: US/10/989,767A
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 699
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-699

Query Match      100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 5
US-10-757-832-52
; Sequence 52, Application US/10757832
; Publication No. US20060024319A2
; GENERAL INFORMATION:
; APPLICANT: VIRGIN, HERBERT W.
; TITLE OF INVENTION: MURINE CALICIVIRUS
; FILE REFERENCE: 56029-45752
; CURRENT APPLICATION NUMBER: US/10/757,832
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 60/440,016
; PRIOR FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Illustrative MNV-1 ORF1 motif
US-10-757-832-52

Query Match      100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 6
US-10-909-957-10
; Sequence 10, Application US/10909957
; Publication No. US20060024332A1
; GENERAL INFORMATION:
; APPLICANT: Waters, Wade R
; APPLICANT: Palmer, Mitchell V
; APPLICANT: Minion, Frank C
; TITLE OF INVENTION: Recombinant ESAT-6:CFP-10 Fusion Protein Useful for
; TITLE OF INVENTION: Specific Diagnosis of Tuberculosis
; FILE REFERENCE: 0072.04 - Waters et al.
; CURRENT APPLICATION NUMBER: US/10/909,957
; CURRENT FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Signal Peptide
US-10-909-957-10

Query Match      100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 7
US-10-962-951-4
; Sequence 4, Application US/10962951
; Publication No. US20060029610A1
; GENERAL INFORMATION:
; APPLICANT: Argon, Yair
; APPLICANT: Gidalevitz, Tali
; APPLICANT: Biswas, Chhanda
; APPLICANT: Simen, Birgitte B.
; APPLICANT: Wanderling, Sherry
; APPLICANT: Ostrovsky, Olga
; TITLE OF INVENTION: GRP94-BASED COMPOSITIONS AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 3460-CHOP.C-2060US
; CURRENT APPLICATION NUMBER: US/10/962,951
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US/10/844,711
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/469,723
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/477,990
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: 60/478,149
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: 60/556,362
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: 60/566,363
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
```

Mon Mar 20 08:51:26 2006

us-09-673-707-9.rapbn

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ER retrieval signal
US-10-962-951-4

Query Match          100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 8
US-10-537-061-11
; Sequence 11, Application US/10537061
; Publication No. US20060051359A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
; FILE REFERENCE: (FV)-P38 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTOM
; CURRENT APPLICATION NUMBER: US/10/537,061
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: PCT/US03/038227
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-537-061-11

Query Match          100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 9
US-11-042-988-14
; Sequence 14, Application US/11042988
; Publication No. US20050244818A1
; GENERAL INFORMATION:
; APPLICANT: SILICIANO, ROBERT
; APPLICANT: ZHANG, HAILI
; APPLICANT: ZHOU, YAN
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
; FILE REFERENCE: 62760(71699)
; CURRENT APPLICATION NUMBER: US/11/042,988
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-042-988-14

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 10
US-11-057-058-2
; Sequence 2, Application US/11057058
; Publication No. US2005024400A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A C-terminal sequence of a targeting domain
US-11-057-058-2

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 11
US-11-179-844-4
; Sequence 4, Application US/11179844
; Publication No. US20050249738A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Goldenberg, David M.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Immunotoxins Directed Against Malignant Cells
; FILE REFERENCE: 015280-325200US
; CURRENT APPLICATION NUMBER: US/11/179,844
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: US/09/918,887
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US 60/046,895
; PRIOR FILING DATE: 1997-05-02
; PRIOR APPLICATION NUMBER: US 09/071,672
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
```

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; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:carboxy terminal
; OTHER INFORMATION: sequence of rFB4-PE38KDEL and LL2-PE38KDEL chimeric
; OTHER INFORMATION: immunotoxins with Pseudomonas exotoxin A (PE) modified
; OTHER INFORMATION: by KDEL endoplasmic reticulum retention sequence
US-11-179-844-4

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 12
US-11-018-106-1
; Sequence 1, Application US/11018106
; Publication No. US2005025550A1
; GENERAL INFORMATION:
; APPLICANT: IMPERIAL COLLEGE INNOVATIONS LIMITED
; APPLICANT: RAMAKHA, PUNIT
; APPLICANT: GEORGE, ANDREW
; APPLICANT: HASKARD, DORIAN
; APPLICANT: LECHLER, ROBERT
; APPLICANT: DORLING, ANTHONY
; TITLE OF INVENTION: SUPPRESSION OF XENOTRANSPLANT REJECTION
; FILE REFERENCE: REV 1021
; CURRENT APPLICATION NUMBER: US/11/018,106
; CURRENT FILING DATE: 2004-12-20
; PRIOR FILING DATE: US 09/856,322
; PRIOR APPLICATION NUMBER: PCT/GB99/03888
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: GB9825555.7
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: targeting
; OTHER INFORMATION: sequence
US-11-018-106-1

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 13
US-11-069-642-159
; Sequence 159, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3

; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-642-159

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 14
US-11-189-321-8
; Sequence 8, Application US/11189321
; Publication No. US20050272154A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Bio Corporation
; APPLICANT: Wolff, Jon A
; APPLICANT: Hagstrom, James E
; APPLICANT: Buckner, Vladimir G
; APPLICANT: Slattum, Paul M
; TITLE OF INVENTION: Gene Expression with Covalently Modified Polynucleotides
; FILE REFERENCE: Mirus 017.01.1
; CURRENT APPLICATION NUMBER: US/11/189,321
; CURRENT FILING DATE: 2005-07-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-189-321-8

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 15
US-11-019-027-1
; Sequence 1, Application US/11019027
; Publication No. US20050282181A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Wei
; APPLICANT: SHEN, Wenyan
; APPLICANT: ZHOU, Hongxing
; APPLICANT: ZHOU, Chen
; APPLICANT: COSMAN, David J.
; APPLICANT: CARTER, Paul
; APPLICANT: MARTIN, Francis H.
; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES
; FILE REFERENCE: A-890A
; CURRENT APPLICATION NUMBER: US/11/019,027
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; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: retention sequence
; US-11-214-613-97

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 18
US-11-029-188-16
; Sequence 16, Application US/11029188
; Publication No. US20060013832A1
; GENERAL INFORMATION:
; APPLICANT: JUNE, CARL H.
; APPLICANT: THOMPSON, CRAIG B.
; APPLICANT: NABEL, GARY J.
; APPLICANT: GRAY, GARY S.
; APPLICANT: RENNERT, PAUL D.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING PROLIFERATION OF T
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 36119.125 US13
; CURRENT APPLICATION NUMBER: US/11/029,188
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: 08/592,711
; PRIOR FILING DATE: 1996-01-26
; PRIOR APPLICATION NUMBER: 08/435,816
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: 08/403,253
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: 08/253,964
; PRIOR FILING DATE: 1994-06-03
; PRIOR APPLICATION NUMBER: 08/073,223
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: 07/864,866
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/864,807
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/864,805
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/275,433
; PRIOR FILING DATE: 1988-11-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-11-029-188-16

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

US-09-673-707-9.rapbn

; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: 60/605,902
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: 60/531,714
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ER localization signal
; US-11-019-027-1

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 16
US-11-102-883-42
; Sequence 42, Application US/11102883
; Publication No. US20050281816A1
; GENERAL INFORMATION:
; APPLICANT: Lampert, Norbert
; APPLICANT: Cramer, Reto
; APPLICANT: Fluckiger, Sabina
; APPLICANT: Daigle, Isabelle
; TITLE OF INVENTION: Modular Antigen Transporter Molecules (MAT Molecules) for
; TITLE OF INVENTION: Modulating Immune Reactions, Associated Constructs, Methods and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 03100234pa
; CURRENT APPLICATION NUMBER: US/11/102,883
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: EP02022774.0
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/011190
; PRIOR FILING DATE: 2003-10-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: partial sequence form calreticulin
; US-11-102-883-42

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 17
US-11-214-613-97
; Sequence 97, Application US/11214613
; Publication No. US20060005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; US-11-214-613-97
```


Db 1 KDEL 4
|||||

RESULT 19

US-11-141-725-47
; Sequence 47, Application US/11141725
; Publication No. US20060014712A1
; GENERAL INFORMATION:
; APPLICANT: Neuman, Tomas
; TITLE OF INVENTION: Controlled Delivery of Therapeutic Compounds
; FILE REFERENCE: 34211/US/2 (473322-00024)
; CURRENT APPLICATION NUMBER: US/11/141,725
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US 60/575,660
; PRIOR FILING DATE: 2004-05-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-141-725-47

Query Match 100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||||

Db 1 KDEL 4
|||||

RESULT 20

US-11-219-180-12
; Sequence 12, Application US/11219180
; Publication No. US20060026715A1
; GENERAL INFORMATION:
; APPLICANT: HOOD, ELIZABETH
; APPLICANT: HOWARD, JOHN
; TITLE OF INVENTION: COMMERCIAL PRODUCTION OF POLYSACCHARIDE DEGRADING
; FILE REFERENCE: AB0007
; CURRENT APPLICATION NUMBER: US/11/219,180
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/607,098
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 60/340,035
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-219-180-12

Query Match 100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||||

Db 1 KDEL 4
|||||

RESULT 21

US-11-174-413-62

; Sequence 62, Application US/11174413
; Publication No. US20060031962A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Dahlbacka, Glen
; APPLICANT: Elleskaya, I.A.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Hunter-Cevera, Jennie
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Prensail, James
; APPLICANT: Rice, Janet
; APPLICANT: Schnepers, Eric
; APPLICANT: Simmons, Carl R.
; APPLICANT: Torok, Tamas
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Antifungal Polypeptides
; FILE REFERENCE: 035718/293488
; CURRENT APPLICATION NUMBER: US/11/174,413
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: 60/585,267
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Endoplasmic reticulum retention sequence
US-11-174-413-62

Query Match 100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||||

Db 1 KDEL 4
|||||

RESULT 22

US-11-126-817-17
; Sequence 17, Application US/11126817
; Publication No. US20060034834A1
; GENERAL INFORMATION:
; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
; APPLICANT: MARASCO, Wayne
; APPLICANT: MEASHILKAR, Abner
; TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE REACTIONS
; FILE REFERENCE: 47577 C
; CURRENT APPLICATION NUMBER: US/11/126,817
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/09/522,727
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/19563
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/059,339
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: human
US-11-126-817-17

Query Match 100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||||

Db 1 KDEL 4
|||||

; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: ER-RETAINING PEPTIDE, SOURCE UNKNOWN
US-11-081-140-8

Query Match 100.0%; Score 20; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 2 KDEL 5

RESULT 27

US-10-493-909-4
; Sequence 4, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
; TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493,909
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-4

Query Match 100.0%; Score 20; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 3 KDEL 6

RESULT 28

US-11-019-027-58
; Sequence 58, Application US/11019027
; Publication No. US20050282181A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Wei
; APPLICANT: SHEN, Wenyan
; APPLICANT: ZHOU, Hongxing
; APPLICANT: ZHOU, Chen
; APPLICANT: COSMAN, David J.
; APPLICANT: CARTER, Paul
; APPLICANT: MARTIN, Francis H.
; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES
; FILE REFERENCE: A-890A
; CURRENT APPLICATION NUMBER: US/11/019,027
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: 60/605,902
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: 60/531,714
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ER localization signal
US-11-019-027-58

Query Match 100.0%; Score 20; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 3 KDEL 6

RESULT 29

US-11-174-413-63
; Sequence 63, Application US/11174413
; Publication No. US20060031962A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Dahibacka, Glen
; APPLICANT: Elleskaya, I.A.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Hunter-Cevera, Jennie
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnail, James
; APPLICANT: Rice, Janet
; APPLICANT: Schepers, Eric
; APPLICANT: Simmons, Carl R.
; APPLICANT: Torok, Tamas
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Antifungal Polypeptides
; FILE REFERENCE: 035718/293488
; CURRENT APPLICATION NUMBER: US/11/174,413
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: 60/585,267
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Endoplasmic reticulum retention sequence
US-11-174-413-63

Query Match 100.0%; Score 20; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 3 KDEL 6

RESULT 30

US-11-126-817-13
; Sequence 13, Application US/11126817
; Publication No. US20060034834A1
; GENERAL INFORMATION:
; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
; APPLICANT: MARASCO, Wayne
; APPLICANT: MHASHILKAR, Abner
; TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE REACTIONS
; FILE REFERENCE: 47577 C
; CURRENT APPLICATION NUMBER: US/11/126,817
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/09/522,727
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/19563

Mon Mar 20 08:51:26 2006

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;
;
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/059,339
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: human
US-11-126-817-13

Query Match          100.0%; Score 20; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      3 KDEL 6

RESULT 31
US-10-493-909-5
; Sequence 5, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
; TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493,909
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-5

Query Match          100.0%; Score 20; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      4 KDEL 7

RESULT 32
US-11-042-988-16
; Sequence 16, Application US/11042988
; Publication No. US20050244818A1
; GENERAL INFORMATION:
; APPLICANT: SILICIANO, ROBERT
; APPLICANT: ZHANG, HAILI
; APPLICANT: ZHOU, YAN
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
; TITLE OF INVENTION: DRUG RESISTANCE
; FILE REFERENCE: 62760(71699)
; CURRENT APPLICATION NUMBER: US/11/042,988
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT

;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-042-988-16

Query Match          100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      4 KDEL 7

RESULT 33
US-11-214-613-85
; Sequence 85, Application US/11214613
; Publication No. US20060005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDEL fusion peptide
US-11-214-613-85

Query Match          100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      4 KDEL 7

RESULT 34
US-11-214-613-86
; Sequence 86, Application US/11214613
; Publication No. US20060005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: designated KDEL fusion peptide
US-11-214-613-86

Query Match 100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Length 7;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 4 KDEL 7

RESULT 35

US-11-214-613-90
; Sequence 90, Application US/11214613
; Publication No. US2006005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ER retention vector
US-11-214-613-90

Query Match 100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Length 7;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 4 KDEL 7

RESULT 36

US-11-214-613-5
; Sequence 5, Application US/11214613
; Publication No. US2006005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: retention sequence
US-11-214-613-5

Query Match 100.0%; Score 20; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 7 KDEL 10

RESULT 37

US-10-952-535A-32
; Sequence 32, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-952-535A-32

Query Match 100.0%; Score 20; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 12 KDEL 15

RESULT 38

US-11-206-138-2
; Sequence 2, Application US/11206138
; Publication No. US20060039919A1
; GENERAL INFORMATION:
; APPLICANT: HealthBanks Biotech CO. LTD.
; TITLE OF INVENTION: Fusion protein for inhibiting cervical cancer
; FILE REFERENCE: P7819/0613
; CURRENT APPLICATION NUMBER: US/11/206,138
; CURRENT FILING DATE: 2005-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
US-11-206-138-2

Query Match 100.0%; Score 20; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 7 KDEL 10

RESULT 39

US-11-193-654-18

```
; Sequence 18, Application US/11193654
; Publication No. US20060019316A1
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Bahiyat, Bassil L.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-A/RT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/11/193,654
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/09/127,926
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/087,561
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-193-654-18

Query Match      100.0%; Score 20; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      15 KDEL 18

RESULT 40
US-11-096-568A-9747
; Sequence 9747, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9747
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(38)
; OTHER INFORMATION: Ceres Seq. ID no. 12619229
US-11-096-568A-9747

Query Match      100.0%; Score 20; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      35 KDEL 38
```

```
; Sequence 34, Application US/11245400
; Publication No. US20060040357A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasehkar
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
; TITLE OF INVENTION: Associated Antigen Molecules, Aminotransferase
; TITLE OF INVENTION: Molecules, ATPase Molecules, Acyltransferase Molecules,
; TITLE OF INVENTION: Pyridoxal-Phosphate Dependant Enzyme Molecules and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/247400
; CURRENT APPLICATION NUMBER: US/11/245,400
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US/10/164,966
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/034,864
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/996,194
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/250,348
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,073
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/253,878
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,338
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/908,928
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,465
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-11-245-400-34

Query Match      100.0%; Score 20; DB 7; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      9 KDEL 12

RESULT 42
US-11-174-413-38
; Sequence 38, Application US/11174413
; Publication No. US20060031962A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Dahlbacka, Glen
; APPLICANT: Elleskaya, I.A.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Hunter-Cevera, Jennie
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Prensail, James
; APPLICANT: Rice, Janet
; APPLICANT: Schepers, Eric
; APPLICANT: Simmons, Carl R.
```

```
; APPLICANT: Torok, Tamas
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Antifungal Polypeptides
; FILE REFERENCE: 035718/293488
; CURRENT APPLICATION NUMBER: US/11/174,413
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: 60/585,267
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of SEQ ID NO:1 (LEML 5220)
; OTHER INFORMATION: joined with a carboxy-terminal KDEL sequence (SEQ
; OTHER INFORMATION: ID NO:62)
US-11-174-413-38

Query Match      100.0%; Score 20; DB 7; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      56 KDEL 59

RESULT 43
US-11-195-459-6
; Sequence 6, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Meeley, Robert
; APPLICANT: Hantke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-6

Query Match      100.0%; Score 20; DB 7; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      47 KDEL 50

RESULT 44
US-10-467-657-414
; Sequence 414, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
```

```
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 414
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-414

Query Match      100.0%; Score 20; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      17 KDEL 20

RESULT 45
US-11-022-562-224
; Sequence 224, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 224
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-11-022-562-224

Query Match      100.0%; Score 20; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      27 KDEL 30

RESULT 46
US-10-986-501-200
; Sequence 200, Application US/10986501
; Publication No. US2005024845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
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; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-200

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 58 KDEL 61

RESULT 47
US-10-517-696-99
; Sequence 99, Application US/10517696
; Publication No. US20060051759A1
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: US/10/517,696
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,327
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-517-696-99

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 46 KDEL 49

RESULT 48
US-10-986-501-125
; Sequence 125, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (51)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-986-501-125

Query Match 100.0%; Score 20; DB 6; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 39 KDEL 42

RESULT 49
US-11-096-568A-19081
; Sequence 19081, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19081
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(111)
; OTHER INFORMATION: Ceres Seq. ID no. 12368808
US-11-096-568A-19081

Query Match 100.0%; Score 20; DB 7; Length 111;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 Db 33 KDEL 36

RESULT 50
 US-10-467-657-6306
 ; Sequence 6306, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 6306
 ; LENGTH: 112
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-6306

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Qy 1 KDEL 4
 Db 73 KDEL 76

Search completed: March 20, 2006, 07:53:54
 Job time : 8.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:41 ; Search time 401.5 Seconds
(without alignments)
13.768 Million cell-updates/sec

Title: US-09-673-707-9
Perfect score: 20
Sequence: 1 KDEL 4

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Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	4	1	PCT-US00-06588-66	Sequence 66, Appl
2	20	100.0	4	1	PCT-US00-13684-22	Sequence 22, Appl
3	20	100.0	4	1	PCT-US00-25559-111	Sequence 111, App
4	20	100.0	4	1	PCT-US00-32583-9	Sequence 9, Appli
5	20	100.0	4	1	PCT-US01-06769-7	Sequence 7, Appli
6	20	100.0	4	1	PCT-US01-41430-10	Sequence 10, Appl
7	20	100.0	4	1	PCT-US01-43588-97	Sequence 97, Appl
8	20	100.0	4	1	PCT-US01-43588A-97	Sequence 97, Appl
9	20	100.0	4	1	PCT-US02-02814-25	Sequence 25, Appl
10	20	100.0	4	1	PCT-US02-02814-35	Sequence 35, Appl
11	20	100.0	4	1	PCT-US02-10132-5	Sequence 5, Appli
12	20	100.0	4	1	PCT-US02-13008-23	Sequence 23, Appl
13	20	100.0	4	1	PCT-US02-15520-43	Sequence 43, Appl
14	20	100.0	4	1	PCT-US02-16391-15	Sequence 15, Appl
15	20	100.0	4	1	PCT-US02-16906-17	Sequence 17, Appl
16	20	100.0	4	1	PCT-US02-19297-163	Sequence 163, App
17	20	100.0	4	1	PCT-US02-21677-31	Sequence 31, Appl
18	20	100.0	4	1	PCT-US02-21677-41	Sequence 41, Appl
19	20	100.0	4	1	PCT-US02-21677-118	Sequence 118, App
20	20	100.0	4	1	PCT-US02-26837-33	Sequence 33, Appl
21	20	100.0	4	1	PCT-US02-27628-30	Sequence 30, Appl
22	20	100.0	4	1	PCT-US02-27628A-30	Sequence 30, Appl
23	20	100.0	4	1	PCT-US02-29560-411	Sequence 411, App
24	20	100.0	4	1	PCT-US02-29560A-411	Sequence 411, App
25	20	100.0	4	1	PCT-US02-30118-8	Sequence 8, Appli
26	20	100.0	4	1	PCT-US02-30316-5	Sequence 5, Appli
27	20	100.0	4	1	PCT-US02-38763-4	Sequence 4, Appli
28	20	100.0	4	1	PCT-US02-38849-8	Sequence 8, Appli
29	20	100.0	4	1	PCT-US02-41158-26	Sequence 26, Appl
30	20	100.0	4	1	PCT-US02-41158A-26	Sequence 26, Appl
31	20	100.0	4	1	PCT-US02-41510-102	Sequence 102, App
32	20	100.0	4	1	PCT-US03-04631-23	Sequence 23, Appl
33	20	100.0	4	1	PCT-US03-10081-4	Sequence 4, Appli
34	20	100.0	4	1	PCT-US03-10630-3	Sequence 3, Appli
35	20	100.0	4	1	PCT-US03-10630A-3	Sequence 3, Appli
36	20	100.0	4	1	PCT-US03-15809-26	Sequence 26, Appl
37	20	100.0	4	1	PCT-US03-16360-3	Sequence 3, Appli
38	20	100.0	4	1	PCT-US03-18373-30	Sequence 30, Appl
39	20	100.0	4	1	PCT-US03-18373A-30	Sequence 30, Appl
40	20	100.0	4	1	PCT-US03-23691-262	Sequence 262, App
41	20	100.0	4	1	PCT-US03-32968-33	Sequence 33, Appl
42	20	100.0	4	1	PCT-US03-35088A-18	Sequence 18, Appl
43	20	100.0	4	1	PCT-US03-38227-11	Sequence 11, Appl
44	20	100.0	4	1	PCT-US03-39476-5	Sequence 5, Appli
45	20	100.0	4	1	PCT-US04-08866-1955	Sequence 1955, Ap
46	20	100.0	4	1	PCT-US04-10059-103	Sequence 103, App
47	20	100.0	4	1	PCT-US04-11481-9	Sequence 9, Appli
48	20	100.0	4	1	PCT-US04-11482-9	Sequence 9, Appli
49	20	100.0	4	1	PCT-US04-23191-12	Sequence 12, Appl
50	20	100.0	4	1	PCT-US04-23192-12	Sequence 12, Appl
51	20	100.0	4	1	PCT-US04-41020A-73	Sequence 73, Appl
52	20	100.0	4	1	PCT-US04-41023A-89	Sequence 89, Appl
53	20	100.0	4	1	PCT-US05-01382-52	Sequence 52, Appl
54	20	100.0	4	1	PCT-US05-16746-18	Sequence 18, Appl
55	20	100.0	4	1	PCT-US05-22321-10	Sequence 10, Appl


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Db      1 KDEL 4

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; Sequence 111, Application PC/TUS0025559
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013W01
; CURRENT APPLICATION NUMBER: PCT/US00/25559
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/25559
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-25559-111

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
PCT-US00-32583-9
; Sequence 9, Application PC/TUS0032583
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H1, A NOVEL IMMUNOREGULATORY MOLECULE
; FILE REFERENCE: 07039-220W01
; CURRENT APPLICATION NUMBER: PCT/US00/32583
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 09/649,108
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/451,291
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Rattus rattus
PCT-US00-32583-9

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
PCT-US01-06769-7
; Sequence 7, Application PC/TUS0106769
; GENERAL INFORMATION:
; APPLICANT: Mayo Medical Ventures
; TITLE OF INVENTION: h87-H2, A NOVEL CO-STIMULATORY MOLECULE
; FILE REFERENCE: 07039-202W01
; CURRENT APPLICATION NUMBER: PCT/US01/06769
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/186,519
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Rattus norvegicus
PCT-US01-06769-7

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
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Db      1 KDEL 4

RESULT 6
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; Sequence 10, Application PC/TUS0141430
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219W01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Rattus norvegicus
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Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
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Db      1 KDEL 4

RESULT 7
PCT-US01-43588-97
; Sequence 97, Application PC/TUS0143588
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; FILE REFERENCE: GC648-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/43588
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 4
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: retention sequence
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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

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; Sequence 97, Application PC/TUS0143588A
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/43588A
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,608
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 4
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; ORGANISM: Artificial Sequence
; FEATURE:
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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
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; Sequence 25, Application PC/TUS0202814
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice (U.S. Only)
; APPLICANT: Smith, Ernest S. (U.S. Only)
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: PCT/US02/02814
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Endoplasmic reticulum sequence from calreticulin
PCT-US02-02814-25

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 10
PCT-US02-02814-35
; Sequence 35, Application PC/TUS0202814
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice (U.S. Only)
; APPLICANT: Smith, Ernest S. (U.S. Only)
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: PCT/US02/02814
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heterologous signal sequence for the endoplasmic reticulum
PCT-US02-02814-35

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 11
PCT-US02-10132-5
; Sequence 5, Application PC/TUS0210132
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Rubert, Rene S.
; APPLICANT: Morrison, Karen J.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 238P1B2 USEFUL IN TREATMENT AND DETECTION OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 51158-20065.40
; CURRENT APPLICATION NUMBER: PCT/US02/10132
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8913
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
PCT-US02-10132-5
```

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-US02-15520-43

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 12
PCT-US02-13008-23
; Sequence 23, Application PC/TUS0213008
; GENERAL INFORMATION:
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION OF
; FILE REFERENCE: HMV-056.25
; CURRENT APPLICATION NUMBER: PCT/US02/13008
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/285,509
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Calreticulin
; OTHER INFORMATION: targeting sequence
PCT-US02-13008-23

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 13
PCT-US02-15520-43
; Sequence 43, Application PC/TUS0215520
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Faris
; APPLICANT: Arthur B. Raitano
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Douglas Saffran
; APPLICANT: Wangmao Ge
; APPLICANT: Pia M. Challita-Eid
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
; TITLE OF INVENTION: ENTITLED 101P3a11 or PHOR-1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.46
; CURRENT APPLICATION NUMBER: PCT/US02/15520
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 10/017,066
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 10/001,469
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
```

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-US02-15520-43

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 14
PCT-US02-16391-15
; Sequence 15, Application PC/TUS0216391
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: ATTRACTIN/MAHOGANY-LIKE POLYPEPTIDES, POLYNUCLEOTIDES, ANTIBODI
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 3224-WO
; CURRENT APPLICATION NUMBER: PCT/US02/16391
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/293,608
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/324,626
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Localization Sequence
PCT-US02-16391-15

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 15
PCT-US02-16906-17
; Sequence 17, Application PC/TUS0216906
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Dirk, Anderson M.
; APPLICANT: Marken, John S.
; TITLE OF INVENTION: SIGLEC-12 POLYPEPTIDES, POLYNUCLEOTIDES, AND METHODS OF USE THERE
; FILE REFERENCE: 3290-WO
; CURRENT APPLICATION NUMBER: PCT/US02/16906
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/294,199
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Localization sequence
PCT-US02-16906-17

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 16
PCT-US02-19297-163
; Sequence 163, Application PC/TUS0219297
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420PC
; CURRENT APPLICATION NUMBER: PCT/US02/19297
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/317,544
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 163
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:KDEL
; OTHER INFORMATION: endoplasmic reticulum retention sequence
PCT-US02-19297-163

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 17
PCT-US02-21677-31
; Sequence 31, Application PC/TUS0221677
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Wei, Chungwen
; APPLICANT: Smith, Ernest
; TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic Cel
; FILE REFERENCE: 1821.009PC05
; CURRENT APPLICATION NUMBER: PCT/US02/21677
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/298,095
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/271,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/263,200
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,225
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: targeting sequence
PCT-US02-21677-31

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 18
PCT-US02-21677-41
; Sequence 41, Application PC/TUS0221677
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Wei, Chungwen
; APPLICANT: Smith, Ernest
; TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic Ce
; FILE REFERENCE: 1821.009PC05
; CURRENT APPLICATION NUMBER: PCT/US02/21677
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/298,095
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/271,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/263,200
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,225
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: signal sequence
PCT-US02-21677-41

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 19
PCT-US02-21677-118
; Sequence 118, Application PC/TUS0221677
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Wei, Chungwen
; APPLICANT: Smith, Ernest
; TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic C
; FILE REFERENCE: 1821.009PC05
; CURRENT APPLICATION NUMBER: PCT/US02/21677
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/298,095
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/271,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/263,200
; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: 60/263,225
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: localization signal
PCT-US02-21677-118

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 20
PCT-US02-26837-33
; Sequence 33, Application PC/TUS0226837
; GENERAL INFORMATION:
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Physalia Fluorescent Proteins
; FILE REFERENCE: FP-71663-PC/TAL/AXG
; CURRENT APPLICATION NUMBER: PCT/US02/26837
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/314,378
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-26837-33

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 21
PCT-US02-27628-30
; Sequence 30, Application PC/TUS0227628
; GENERAL INFORMATION:
; APPLICANT: Rossi, Alex
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High Th
; FILE REFERENCE: A-70882/RMS/AMS
; CURRENT APPLICATION NUMBER: PCT/US02/27628
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/316,723
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-27628-30

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 22
PCT-US02-27628A-30
; Sequence 30, Application PC/TUS0227628A
; GENERAL INFORMATION:
; APPLICANT: RIGEL PHARMACEUTICALS, INC.
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High
; FILE REFERENCE: FP-70882-PC/RMS/AMS
; CURRENT APPLICATION NUMBER: PCT/US02/27628A
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/316,723
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 10/053,355
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-27628A-30

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

RESULT 23
PCT-US02-29560-411
; Sequence 411, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; CURRENT FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 411
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDEL endoplasmic reticulum retention sequence
PCT-US02-29560-411

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||
Db 1 KDEL 4

Mon Mar 20 08:51:26 2006

```

; Sequence 5, Application PC/TUS0230316
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Salvatore, Giuliana
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100PC
; CURRENT APPLICATION NUMBER: PCT/US02/30316
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:carboxyl
; OTHER INFORMATION: terminus addition to maintain ability of the
; OTHER INFORMATION: construct to translocate to cytosol
; PCT-US02-30316-5

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 27
PCT-US02-38763-4
; Sequence 4, Application PC/TUS0238763
; GENERAL INFORMATION:
; APPLICANT: PRODIGENE, INC.
; TITLE OF INVENTION: METHODS FOR THE COST-EFFECTIVE SACCHARIFICATION OF
; TITLE OF INVENTION: LIGNOCELLULOSIC BIOMASS
; FILE REFERENCE: 10038 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/38763
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 60/340,035
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic KDEL
; OTHER INFORMATION: motif
; PCT-US02-38763-4

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 28
PCT-US02-38849-8
; Sequence 8, Application PC/TUS0238849
; GENERAL INFORMATION:

```

```

; Sequence 411, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 411
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDEL endoplasmic reticulum retention sequence
; PCT-US02-29560A-411

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 25
PCT-US02-30118-8
; Sequence 8, Application PC/TUS0230118
; GENERAL INFORMATION:
; APPLICANT: PRODIGENE, INC.
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN PLANTS
; FILE REFERENCE: C-36-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/30118
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/324,308
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide motif
; PCT-US02-30118-8

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 26
PCT-US02-30316-5

```

; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
; TITLE OF INVENTION: ANTIBODY TO LATENT MEMBRANE PROTEINS AND USES THEREOF
; FILE REFERENCE: 52141-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/38849
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,294
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative motif
PCT-US02-38849-8

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 29

PCT-US02-41158-26
; Sequence 26, Application PC/TUS0241158
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; APPLICANT: BAUM, Peter R.
; TITLE OF INVENTION: C-Type Lectin Polypeptide, Polynucleotide and Methods of Making a
; FILE REFERENCE: 3303-WO
; CURRENT APPLICATION NUMBER: PCT/US02/41158
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,001
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Localization Sequence
PCT-US02-41158-26

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 30

PCT-US02-41158A-26
; Sequence 26, Application PC/TUS0241158A
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; APPLICANT: BAUM, Peter R.
; TITLE OF INVENTION: C-Type Lectin Polypeptide, Polynucleotide and Methods of Making a
; FILE REFERENCE: 3303-WO
; CURRENT APPLICATION NUMBER: PCT/US02/41158A
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/342,001
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Localization Sequence
PCT-US02-41158A-26

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 31

PCT-US02-41510-102
; Sequence 102, Application PC/TUS0241510
; GENERAL INFORMATION:
; APPLICANT: GLYCOPI, INC.
; TITLE OF INVENTION: METHODS TO ENGINEER MAMMALIAN-TYPE CARBOHYDRATE
; FILE REFERENCE: GFI/102 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/41510
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/344,169
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: retention signal peptide
PCT-US02-41510-102

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 32

PCT-US03-04631-23
; Sequence 23, Application PC/TUS0304631
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-Lepain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESP
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: PCT/US03/04631
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: synthetic construct
PCT-US03-04631-23

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 33
PCT-US03-10081-4
; Sequence 4, Application PC/TUS0310081
; GENERAL INFORMATION:
; TITLE OF INVENTION: Selective Genetics, Inc.
; APPLICANT: Abbott, Robert
; APPLICANT: Larocca, David
; APPLICANT: Baird, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PORTAL
; FILE REFERENCE: 760100.460PC
; CURRENT APPLICATION NUMBER: PCT/US03/10081
; CURRENT FILING DATE: 2003-04-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ER retention sequence
PCT-US03-10081-4

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 34
PCT-US03-10630-3
; Sequence 3, Application PC/TUS0310630
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015
; CURRENT APPLICATION NUMBER: PCT/US03/10630
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US03-10630-3

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 35
PCT-US03-10630A-3
; Sequence 3, Application PC/TUS0310630A
; GENERAL INFORMATION:
; APPLICANT: Kimberly A. Kelly
; APPLICANT: David A. Jones
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015US1

```

```

; CURRENT APPLICATION NUMBER: PCT/US03/10630A
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/US03/10630
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US03-10630A-3

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 36
PCT-US03-15809-26
; Sequence 26, Application PC/TUS0315809
; GENERAL INFORMATION:
; APPLICANT: Henry, Lu
; APPLICANT: Huang, Peiyong
; APPLICANT: Kinsella, Todd
; APPLICANT: Martinez, Anthony
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AND IDENTIFYING ANTI-HCV
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: RIGL-016WO
; CURRENT APPLICATION NUMBER: PCT/US03/15809
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 10/152,163
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-15809-26

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 37
PCT-US03-16360-3
; Sequence 3, Application PC/TUS0316360
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Rozema, David
; APPLICANT: Wolff, Jon
; APPLICANT: Wakefield, Darren
; APPLICANT: Ekena, Kirk
; APPLICANT: Hagstrom, James
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction
; FILE REFERENCE: MC.035.01.1
; CURRENT APPLICATION NUMBER: PCT/US03/16360
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4

```

; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-16360-3

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|
|
|
|
Db 1 KDEL 4

RESULT 38

PCT-US03-18373-30

; Sequence 30, Application PC/TUS0318373

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira H.

; APPLICANT: Nagata, Satoshi

; APPLICANT: Onda, Masanori

; APPLICANT: Numata, Yoshito

; APPLICANT: Santora, Kenneth

; APPLICANT: Beers, Richard

; APPLICANT: Kreitman, Robert

; APPLICANT: Sinha, Abhishek

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for

; TITLE OF INVENTION: Use in Immunotoxins

; FILE REFERENCE: 015280-464100PC

; CURRENT APPLICATION NUMBER: PCT/US03/18373

; CURRENT FILING DATE: 2003-06-09

; PRIOR APPLICATION NUMBER: US 60/387,293

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/411,032

; PRIOR FILING DATE: 2002-09-16

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 30

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas

; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition

PCT-US03-18373-30

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|
|
|
|
Db 1 KDEL 4

RESULT 39

PCT-US03-18373A-30

; Sequence 30, Application PC/TUS0318373A

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira H.

; APPLICANT: Nagata, Satoshi

; APPLICANT: Onda, Masanori

; APPLICANT: Numata, Yoshito

; APPLICANT: Santora, Kenneth

; APPLICANT: Beers, Richard

; APPLICANT: Kreitman, Robert

; APPLICANT: Sinha, Abhishek

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence universally recognized as signals for protein
; OTHER INFORMATION: retention in the endoplasmic reticulum (ER)
PCT-US03-32968-33

```

```

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KDEL 4
    ||||
Db 1 KDEL 4

```

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RESULT 42
PCT-US03-35088A-18
; Sequence 18, Application PC/TUS0335088A
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Baker, Brenda
; APPLICANT: Eldrup, Ann
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Griffey, Richard H.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Conjugated Oligomeric Compounds and Their Use in Gene
; TITLE OF INVENTION: Modulation
; FILE REFERENCE: ISIC0009-500
; CURRENT APPLICATION NUMBER: PCT/US03/35088A
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 10/616,241
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/423,760
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically Synthesized Peptide
PCT-US03-35088A-18

```

```

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KDEL 4
    ||||
Db 1 KDEL 4

```

```

RESULT 43
PCT-US03-38227-11
; Sequence 11, Application PC/TUS0338227
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
; TITLE OF INVENTION: (FV)-PE38 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTOM
; FILE REFERENCE: 4239-67287
; CURRENT APPLICATION NUMBER: PCT/US03/38227
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02

```

```

; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
PCT-US03-38227-11

```

```

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 KDEL 4
    ||||
Db 1 KDEL 4

```

```

RESULT 44
PCT-US03-39476-5
; Sequence 5, Application PC/TUS0339476
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Eglund, Kristi A.
; APPLICANT: Vincent, James J.
; APPLICANT: Lee, Byungkook
; APPLICANT: Strausberg, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: BASE, a New Cancer Gene, and Uses Thereof
; FILE REFERENCE: 015280-475100PC
; CURRENT APPLICATION NUMBER: PCT/US03/39476
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,531
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:carboxyl
; OTHER INFORMATION: terminus addition sequence
PCT-US03-39476-5

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Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 KDEL 4
    ||||
Db 1 KDEL 4

```

```

RESULT 45
PCT-US04-08866-1955
; Sequence 1955, Application PC/TUS0408866
; GENERAL INFORMATION:
; APPLICANT: Dana Farber Cancer Institute, Inc.
; TITLE OF INVENTION: GENE EXPRESSION IN BREAST CANCER
; FILE REFERENCE: 00530-116W01
; CURRENT APPLICATION NUMBER: PCT/US04/08866
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,735
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 1955
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1955
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-08866-1955

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Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 46

PCT-US04-10059-103
; Sequence 103, Application PC/TUS0410059
; GENERAL INFORMATION:
; APPLICANT: INTRADIGM CORPORATION
; TITLE OF INVENTION: TARGETS FOR TUMOR GROWTH INHIBITION
; FILE REFERENCE: 38147-0055
; CURRENT APPLICATION NUMBER: PCT/US04/10059
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 60/458,948
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 60/489,504
; PRIOR FILING DATE: 2003-07-24
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 103
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US04-10059-103

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 47

PCT-US04-11481-9
; Sequence 9, Application PC/TUS0411481
; GENERAL INFORMATION:
; APPLICANT: MedImmune, Inc.
; TITLE OF INVENTION: EphA2 and Hypoproliferative Cell Disorders and Epithelial and End
; FILE REFERENCE: 10271-058-228
; CURRENT APPLICATION NUMBER: PCT/US04/11481
; CURRENT FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 60/462,009
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-11481-9

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 48

PCT-US04-11482-9
; Sequence 9, Application PC/TUS0411482
; GENERAL INFORMATION:
; APPLICANT: MedImmune, Inc.
; TITLE OF INVENTION: EphA2 and Hyperproliferative Cell Disorders
; FILE REFERENCE: 10271-060-228
; CURRENT APPLICATION NUMBER: PCT/US04/11482
; CURRENT FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 60/462,024
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-11482-9

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 49

PCT-US04-23191-12
; Sequence 12, Application PC/TUS0423191
; GENERAL INFORMATION:
; APPLICANT: MedImmune, Inc.
; TITLE OF INVENTION: DIAGNOSIS OF PRE-CANCEROUS CONDITIONS
; FILE REFERENCE: 10271-131-228
; CURRENT APPLICATION NUMBER: PCT/US04/23191
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: 60/489,035
; PRIOR FILING DATE: 2003-07-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: localization signal used to direct intrabody to endoplasmic ret
PCT-US04-23191-12

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 50

PCT-US04-23192-12
; Sequence 12, Application PC/TUS0423192
; GENERAL INFORMATION:
; APPLICANT: MedImmune, Inc.
; TITLE OF INVENTION: TREATMENT OF PRE-CANCEROUS CONDITIONS
; FILE REFERENCE: 10271-110-228
; CURRENT APPLICATION NUMBER: PCT/US04/23192
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: 60/489,035
; PRIOR FILING DATE: 2003-07-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12

Mon Mar 20 08:51:26 2006

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; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Localization signal used to direct intrabody to endoplasmic retic
PCT-US04-23192-12

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
      ||||
Db      1 KDEL 4

Search completed: March 20, 2006, 08:10:46
Job time : 403.5 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:40 ; Search time 17.5 Seconds
(without alignments)
21.955 Million cell updates/sec

Title: US-09-673-707-9

Perfect score: 20

Sequence: 1 KDEEL 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 443638 seqs, 96052105 residues

Total number of hits satisfying chosen parameters: 443638

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Pending_Patents_AA_New.*

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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*

7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*

8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	4	1	PCT-US05-38666-9
2	20	100.0	4	1	PCT-US05-38667-9
3	20	100.0	4	1	PCT-US05-38668-81
4	20	100.0	4	1	PCT-US05-39091-268
5	20	100.0	4	1	PCT-US05-31269A-30
6	20	100.0	4	1	PCT-US05-21612-262
7	20	100.0	4	1	PCT-US05-35802-3
8	20	100.0	4	1	PCT-US04-04340-9
9	20	100.0	4	1	PCT-US04-41023B-89
10	20	100.0	4	5	US-09-892-591A-6
11	20	100.0	4	6	US-11-259-133-81
12	20	100.0	4	6	US-11-259-266-9
13	20	100.0	4	6	US-11-259-267-9
14	20	100.0	4	6	US-11-108-088-70
15	20	100.0	4	6	US-11-263-230-268
16	20	100.0	4	6	US-11-240-432-6
17	20	100.0	4	6	US-11-055-181-7
18	20	100.0	4	6	US-11-312-319-3
19	20	100.0	4	6	US-11-326-148-16
20	20	100.0	4	6	US-11-324-947-44
21	20	100.0	4	6	US-11-053-045-1
22	20	100.0	4	6	US-11-046-590A-12
23	20	100.0	4	6	US-11-154-103-26
24	20	100.0	4	6	US-11-334-622-49
25	20	100.0	4	6	US-11-244-348A-3
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 81, Appli
					Sequence 268, App
					Sequence 30, Appli
					Sequence 262, App
					Sequence 3, Appli
					Sequence 9, Appli
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					Sequence 6, Appli
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Sequence 20562, A
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Sequence 1338, Ap
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4 6 US-11-344-466-6
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4 6 US-11-361-631-24
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4 6 US-10-565-771-12
4 6 US-10-147-368B-43
4 6 US-10-533-266-2
4 6 US-10-500-264-1
4 6 US-10-189-360A-42
4 6 US-10-428-339B-42
4 7 US-11-368-804-52
4 7 US-11-271-235-6
6 6 US-11-335-891-113
6 8 US-60-773-847-38
8 1 PCT-US04-04340-108
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9 6 US-10-537-642-272
15 1 PCT-US05-40707-26
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53 7 US-11-360-355-138406
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92 6 US-10-953-349-18743

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103	20	100.0	97	6	US-10-953-349-7271	Sequence 7271, Ap
104	20	100.0	98	6	US-60-658-984A-13272	Sequence 13272, A
105	20	100.0	99	8	US-10-276-817B-12408	Sequence 12408, A
106	20	100.0	100	6	PCT-US05-14635-44	Sequence 44, Appl
107	20	100.0	101	6	US-10-953-349-20438	Sequence 20438, A
108	20	100.0	102	1	PCT-US05-23326-1369	Sequence 1369, Ap
109	20	100.0	103	8	US-60-658-984A-14664	Sequence 14664, Ap
110	20	100.0	104	8	US-11-360-355-134285	Sequence 134285, A
111	20	100.0	105	6	US-10-953-349-18216	Sequence 18216, A
112	20	100.0	106	6	US-11-360-355-164392	Sequence 164392,
113	20	100.0	107	1	PCT-US05-14635-24	Sequence 24, Appl
114	20	100.0	108	1	US-11-360-355-143860	Sequence 143860,
115	20	100.0	109	7	US-11-360-355-142924	Sequence 142924,
116	20	100.0	110	7	US-11-360-355-142924	Sequence 142924,
117	20	100.0	111	8	US-60-658-984A-2318	Sequence 2318, Ap
118	20	100.0	112	8	US-60-658-984A-14528	Sequence 14528, A
119	20	100.0	113	1	PCT-US05-14635-26	Sequence 26, Appl
120	20	100.0	114	6	US-10-461-673-14980	Sequence 14980, A
121	20	100.0	115	7	US-11-360-355-147485	Sequence 147485,
122	20	100.0	116	7	US-11-360-355-151083	Sequence 151083,
123	20	100.0	117	7	US-11-360-355-129834	Sequence 129834,
124	20	100.0	118	7	US-11-360-355-134603	Sequence 134603,
125	20	100.0	119	7	US-11-360-355-167225	Sequence 167225,
126	20	100.0	120	8	US-60-658-984A-520	Sequence 520, App
127	20	100.0	121	7	US-11-360-355-129681	Sequence 129681,
128	20	100.0	122	7	US-11-360-355-120658	Sequence 120658,
129	20	100.0	123	8	US-60-658-984A-10754	Sequence 10754, A
130	20	100.0	124	8	US-60-658-984A-20856	Sequence 20856, A
131	20	100.0	125	7	US-11-360-355-155048	Sequence 155048,
132	20	100.0	126	7	US-11-360-355-161084	Sequence 161084,
133	20	100.0	127	7	US-11-360-355-168152	Sequence 168152,
134	20	100.0	128	7	US-60-752-355-50045	Sequence 50045, A
135	20	100.0	129	8	US-60-658-984A-4058	Sequence 4058, Ap
136	20	100.0	130	122	PCT-US05-14635-42	Sequence 42, Appl
137	20	100.0	131	6	US-10-953-349-20437	Sequence 20437, A
138	20	100.0	132	7	US-11-360-355-126836	Sequence 126836,
139	20	100.0	133	8	US-60-658-984A-9166	Sequence 9166, Ap
140	20	100.0	134	8	US-60-658-984A-11892	Sequence 11892, A
141	20	100.0	135	8	US-60-658-984A-10786	Sequence 10786, A
142	20	100.0	136	8	US-60-658-984A-13100	Sequence 13100, A
143	20	100.0	137	6	US-11-045-004-1269	Sequence 1269, Ap
144	20	100.0	138	1	PCT-US05-23326-1365	Sequence 1365, Ap
145	20	100.0	139	1	PCT-US05-23326-1366	Sequence 1366, Ap
146	20	100.0	140	1	PCT-US05-23326-1367	Sequence 1367, Ap
147	20	100.0	141	1	PCT-US05-23326-1368	Sequence 1368, Ap
148	20	100.0	142	7	US-11-360-355-152058	Sequence 152058,
149	20	100.0	143	6	US-10-276-817B-13132	Sequence 13132, A
150	20	100.0	144	7	US-11-360-355-125331	Sequence 125331,

ALIGNMENTS

RESULT 1
PCT-US05-38666-9
; Sequence 9, Application PC/TUS0538666
; GENERAL INFORMATION:
; APPLICANT: MedImmune
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; TITLE OF INVENTION: Use of Modulators of EphA2 and EphrinA1 for the Treatment and Pre
; TITLE OF INVENTION: of Infections
; FILE REFERENCE: EP350PCT
; CURRENT APPLICATION NUMBER: PCT/US05/38666
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 60/622,489
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 60/705,705
; PRIOR FILING DATE: 2005-08-03

; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-38666-9

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 2

PCT-US05-38667-9
; Sequence 9, Application PC/TUS0538667
; GENERAL INFORMATION:
; APPLICANT: MedImmune
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; TITLE OF INVENTION: Modulators of EphA2 and EphrinA1 for the Treatment of
; TITLE OF INVENTION: Fibrosis-Related Disease
; FILE REFERENCE: EP301PCT
; CURRENT APPLICATION NUMBER: PCT/US05/38667
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 60/622,517
; PRIOR FILING DATE: 2004-10-27
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-38667-9

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 3

PCT-US05-38668-81
; Sequence 81, Application PC/TUS0538668
; GENERAL INFORMATION:
; APPLICANT: MedImmune
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; TITLE OF INVENTION: MODULATION OF ANTIBODY SPECIFICITY BY TAILORING THE AFFINITY TO
; TITLE OF INVENTION: COGNATE ANTIGENS
; FILE REFERENCE: EP700PCT
; CURRENT APPLICATION NUMBER: PCT/US05/38668
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 60/622,711
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 60/717,209
; PRIOR FILING DATE: 2005-09-16
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-38668-81

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 4
PCT-US05-39091-268
; Sequence 268, Application PC/TUS0539091
; GENERAL INFORMATION:
; APPLICANT: MedImmune, Inc.
; TITLE OF INVENTION: Methods of Preventing and Treating RSV Infections
; FILE REFERENCE: 10271-174-228
; CURRENT APPLICATION NUMBER: PCT/US05/39091
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: 60/623,821
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/675,724
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/681,233
; PRIOR FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/727,042
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/727,043
; PRIOR FILING DATE: 2005-10-14
; NUMBER OF SEQ ID NOS: 1496
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 268
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: intrabody
PCT-US05-39091-268

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 5
PCT-US05-31269A-30
; Sequence 30, Application PC/TUS0531269A
; GENERAL INFORMATION:
; APPLICANT: Swayze, Eric E.
; APPLICANT: Robinson, Dale E. Jr.
; APPLICANT: Jefferson, Elizabeth Ann
; APPLICANT: Dande, Prasad
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Allerson, Charles
; APPLICANT: Bhat, Balakrishen
; TITLE OF INVENTION: PYRROLIDINYL GROUPS FOR ATTACHING
; FILE REFERENCE: CONJUGATES TO OLIGOMERIC COMPOUNDS
; CURRENT APPLICATION NUMBER: PCT/US05/31269A
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/608,201
; PRIOR FILING DATE: 2004-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Delivery peptide
PCT-US05-31269A-30

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 6
PCT-US05-21612-262
; Sequence 262, Application PC/TUS0521612
; GENERAL INFORMATION:
; APPLICANT: Ceres Inc.
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-109W01
; CURRENT APPLICATION NUMBER: PCT/US05/21612
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: 10/873,679
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target sequence
PCT-US05-21612-262

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 7
PCT-US05-35802-3
; Sequence 3, Application PC/TUS0535802
; GENERAL INFORMATION:
; APPLICANT: Mtnsy, Randall J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMMUNIZING
; FILE REFERENCE: 10901-015-999
; CURRENT APPLICATION NUMBER: PCT/US05/35802
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: 60/616,125
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US05-35802-3

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 8

PCT-US04-04340-9
; Sequence 9, Application PC/TUS0404340
; GENERAL INFORMATION:
; APPLICANT: Antigenics, Inc.
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; FILE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-228
; CURRENT APPLICATION NUMBER: PCT/US04/04340
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated heat shock protein peptide
PCT-US04-04340-9

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 9
PCT-US04-41023B-89
; Sequence 89, Application PC/TUS0441023B
; GENERAL INFORMATION:
; APPLICANT: MedImmune, Inc.
; TITLE OF INVENTION: EphA2, EphA4 and LMW-PTP and Methods of
; FILE OF INVENTION: Treatment of Hyperproliferative Cell Disorders
; FILE REFERENCE: 10271-111-228
; CURRENT APPLICATION NUMBER: PCT/US04/41023B
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: 60/527,154
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 11/004,794
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: 11/004,795
; PRIOR FILING DATE: 2004-12-03
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-41023B-89

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 10
US-09-892-591A-6
; Sequence 6, Application US/09892591A
; GENERAL INFORMATION:

; APPLICANT: Gerngross, Tillman U.
; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
; FILE OF INVENTION: GLYCOPROTEINS
; FILE REFERENCE: GFI 100
; CURRENT APPLICATION NUMBER: US/09/892,591A
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/214,358
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/215,638
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/279,997
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Signal tetrapeptide
US-09-892-591A-6

Query Match 100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 11
US-11-259-133-81
; Sequence 81, Application US/11259133
; GENERAL INFORMATION:
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; TITLE OF INVENTION: MODULATION OF ANTIBODY SPECIFICITY BY TAILORING THE AFFINITY TO
; TITLE OF INVENTION: COGNATE ANTIGENS
; FILE REFERENCE: EP700US
; CURRENT APPLICATION NUMBER: US/11/259,133
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: 60/622,711
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 60/717,209
; PRIOR FILING DATE: 2005-09-16
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-259-133-81

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 12
US-11-259-266-9
; Sequence 9, Application US/11259266
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; TITLE OF INVENTION: Use of Modulators of EphA2 and EphrinA1 for the Treatment and P
; TITLE OF INVENTION: of Infections

; FILE REFERENCE: EP350US
; CURRENT APPLICATION NUMBER: US/11/259,266
; PRIOR FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: 60/622,489
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 60/705,705
; PRIOR FILING DATE: 2005-08-03
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-259-266-9

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 13
US-11-259-267-9
; Sequence 9, Application US/11259267
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; TITLE OF INVENTION: Modulators of EphA2 and EphrinA1 for the Treatment of
; FILE REFERENCE: EP301US
; CURRENT APPLICATION NUMBER: US/11/259,267
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: 60/622,517
; PRIOR FILING DATE: 2004-10-27
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-259-267-9

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 14
US-11-108-088-70
; Sequence 70, Application US/11108088
; GENERAL INFORMATION:
; APPLICANT: DAVIDSON, ROBERT
; APPLICANT: GERNGROSS, TILLMAN
; APPLICANT: WILDT, STEFAN
; APPLICANT: CHOI, BYUNG-KWON
; APPLICANT: NETT, JUERGEN
; APPLICANT: BOBROWICZ, PIOTR
; APPLICANT: HAMILTON, STEPHEN
; TITLE OF INVENTION: PRODUCTION OF GALACTOSYLATED GLYCOPROTEINS IN LOWER
; FILE REFERENCE: GFI-12
; CURRENT APPLICATION NUMBER: US/11/108,088
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/214,358
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/215,638

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/279,997
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US02/41510
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 60/344,169
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/562,424
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 70
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-108-088-70

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 15
US-11-263-230-268
; Sequence 268, Application US/11263230
; GENERAL INFORMATION:
; APPLICANT: Losonsky, Genevieve
; APPLICANT: Connor, Edward M.
; APPLICANT: Young, James F.
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; TITLE OF INVENTION: Methods of Preventing and Treating RSV Infections
; TITLE OF INVENTION: and Related Conditions
; FILE REFERENCE: 10271-174-999
; CURRENT APPLICATION NUMBER: US/11/263,230
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: 60/623,821
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/675,724
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/681,233
; PRIOR FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/718,719
; PRIOR FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: 60/727,042
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/727,043
; PRIOR FILING DATE: 2005-10-14
; NUMBER OF SEQ ID NOS: 1496
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 268
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: intrabody
US-11-263-230-268

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

```

; Sequence 3, Application US/11312319
; GENERAL INFORMATION:
; APPLICANT: Mirus Bio Corporation
; APPLICANT: Rozema, David
; APPLICANT: Wolff, Jon
; APPLICANT: Wakefield, Darren
; APPLICANT: Ekena, Kirk
; APPLICANT: Hagstrom, James
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction
; FILE REFERENCE: Mirus.035.01.3
; CURRENT APPLICATION NUMBER: US/11/312,319
; CURRENT FILING DATE: 2005-12-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-312-319-3

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 19
US-11-326-148-16
; Sequence 16, Application US/11326148
; GENERAL INFORMATION:
; APPLICANT: JUNE, CARL H.
; APPLICANT: THOMPSON, CRAIG B.
; APPLICANT: NABEL, GARY J.
; APPLICANT: GRAY, GARY S.
; APPLICANT: RENNERT, PAUL D.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING PROLIFERATION OF T
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 36119.125 US13
; CURRENT APPLICATION NUMBER: US/11/326,148
; CURRENT FILING DATE: 2006-01-05
; PRIOR APPLICATION NUMBER: US/11/029,188
; PRIOR FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: 08/592,711
; PRIOR FILING DATE: 1996-01-26
; PRIOR APPLICATION NUMBER: 08/435,816
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: 08/403,253
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: 08/253,964
; PRIOR FILING DATE: 1994-06-03
; PRIOR APPLICATION NUMBER: 08/073,223
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: 07/864,866
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/864,807
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/864,805
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/275,433
; PRIOR FILING DATE: 1988-11-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-326-148-16

; Sequence 6, Application US/11240432
; GENERAL INFORMATION:
; APPLICANT: Gerengross, Tillman U.
; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
; TITLE OF INVENTION: GLYCOPROTEINS
; FILE REFERENCE: GFI 100 CON
; CURRENT APPLICATION NUMBER: US/11/240,432
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/892,591
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/214,358
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/215,638
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/279,997
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Signal tetrapeptide
US-11-240-432-6

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 17
US-11-055-181-7
; Sequence 7, Application US/11055181
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY J.
; APPLICANT: DENARDO, GERALD L.
; APPLICANT: BALHORN, RODNEY
; TITLE OF INVENTION: SELECTIVE HIGH-AFFINITY POLYDENTATE LIGANDS AND METHODS OF MAKING
; TITLE OF INVENTION: SUCH
; FILE REFERENCE: 309t-300510US
; CURRENT APPLICATION NUMBER: US/11/055,181
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,444
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic translocation signaling sequence.
US-11-055-181-7

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 18
US-11-326-148-16

```

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 20

US-11-324-947-44
; Sequence 44, Application US/11324947
; GENERAL INFORMATION:
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; APPLICANT: FITCHEN, JOHN H.
; TITLE OF INVENTION: J CHAIN POLYPEPTIDE TARGETING MOLECULE LINKED TO AN IMAGING AGENT
; FILE REFERENCE: EPI3003C
; CURRENT APPLICATION NUMBER: US/11/324,947
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/062,467
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 08/782,480
; PRIOR FILING DATE: 1997-01-10
; PRIOR APPLICATION NUMBER: 09/005,167
; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Intracellular
; OTHER INFORMATION: targeting signal
US-11-324-947-44

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 21

US-11-053-045-1
; Sequence 1, Application US/11053045
; GENERAL INFORMATION:
; APPLICANT: Denescke, Jurgen
; APPLICANT: Jelitto, Edith
; TITLE OF INVENTION: Enhancing Plant Pathogen Resistance via Increasing Bip Levels
; FILE REFERENCE: 9052.94
; CURRENT APPLICATION NUMBER: US/11/053,045
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US/09/868,434
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: GB9827480.6
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: mammalian
US-11-053-045-1

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 22

US-11-046-590A-12
; Sequence 12, Application US/11046590A
; GENERAL INFORMATION:
; APPLICANT: Mirus Bio Corporation
; APPLICANT: Trubetskoy, Vladimir
; APPLICANT: Buckner, Vladimir
; APPLICANT: Wolff, Jon
; APPLICANT: Hagstrom, James
; APPLICANT: Rozema, David
; APPLICANT: Monahan, Sean
; TITLE OF INVENTION: Compositions and Methods for Drug Delivery Using pH Sensitive
; TITLE OF INVENTION: Molecules
; FILE REFERENCE: Mirus.009.05.8
; CURRENT APPLICATION NUMBER: US/11/046,590A
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/095,680
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-046-590A-12

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 23

US-11-154-103-26
; Sequence 26, Application US/11154103
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Translocation signaling sequence.
US-11-154-103-26

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

Db 1 KDEL 4

RESULT 24
US-11-334-622-49
; Sequence 49, Application US/11334622
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/11/334,622
; CURRENT FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: US/09/554,000
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-334-622-49

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 25
US-11-244-348A-3
; Sequence 3, Application US/11244348A
; GENERAL INFORMATION:
; APPLICANT: Misny, Randall J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMMUNIZING
; TITLE OF INVENTION: AGAINST PSEUDOMONAS INFECTION
; FILE REFERENCE: 10901-015-999
; CURRENT APPLICATION NUMBER: US/11/244,348A
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: 60/616,125
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
US-11-244-348A-3

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 26
US-11-211-723-22
; Sequence 22, Application US/11211723
; GENERAL INFORMATION:
; APPLICANT: CLARK, PATRICIA L.
; APPLICANT: EVANS, MICHAEL S.
; APPLICANT: UGRINOV, KRASTYU G.
; APPLICANT: CLARKE, IV, THOMAS F.
; APPLICANT: FRESE, MARC-ANDRE

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 27
US-11-344-466-6
; Sequence 6, Application US/11344466
; GENERAL INFORMATION:
; APPLICANT: Fey, Georg H
; APPLICANT: Peipp, Matthias
; APPLICANT: Schwemmler, Michael
; TITLE OF INVENTION: CD19-Specific Immunotoxin and Treatment Method
; FILE REFERENCE: 59849-8005
; CURRENT APPLICATION NUMBER: US/11/344,466
; CURRENT FILING DATE: 2006-01-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic transport sequence
US-11-344-466-6

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 28
US-11-352-733-6
; Sequence 6, Application US/11352733
; GENERAL INFORMATION:
; APPLICANT: AUBURN UNIVERSITY
; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
; FILE REFERENCE: 1463-PCT-US-00
; CURRENT APPLICATION NUMBER: US/11/352,733
; CURRENT FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: US/09/807,721
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/06274
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-352-733-6

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 29

US-11-361-631-24
; Sequence 24, Application US/11361631

; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Kinsella, Todd
; APPLICANT: Masuda, Esteban
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Liao, X. Charlene
; APPLICANT: Pearsall, Denise
; APPLICANT: Freira, Annabelle
; APPLICANT: Chu, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ALTERED CELLULAR PHENOC
; FILE REFERENCE: A-71158/RMS/DCF
; CURRENT APPLICATION NUMBER: US/11/361,631
; CURRENT FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: US/10/096,339
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/076,624
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-361-631-24

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 30

US-10-432-412A-23
; Sequence 23, Application US/10432412A

; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; TITLE OF INVENTION: Exocoxin A and Type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412A
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain
US-10-432-412A-23

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 31

US-10-565-771-12

; Sequence 12, Application US/10565771
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael S.
; TITLE OF INVENTION: DIAGNOSIS OF PRE-CANCEROUS CONDITIONS
; TITLE OF INVENTION: AND USING PCDF AGENTS
; FILE REFERENCE: 10271-131-999
; CURRENT APPLICATION NUMBER: US/10/565,771
; CURRENT FILING DATE: 2006-01-23
; PRIOR APPLICATION NUMBER: 60/489,035
; PRIOR FILING DATE: 2003-07-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Localization signal used to direct intrabody to endoplasmic ret
US-10-565-771-12

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 32

US-10-147-368B-43

; Sequence 43, Application US/10147368B
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: FARIS, Mary
; APPLICANT: RAITANO, Arthur B.
; APPLICANT: MORRISON, Robert Kendall
; APPLICANT: SAFFRAN, Douglas
; APPLICANT: GE, Wangmao
; APPLICANT: CHALITA-EID, Pia M.
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
; TITLE OF INVENTION: ENTITLED 101P3111 or PHOR-1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.21
; CURRENT APPLICATION NUMBER: US/10/147,368B
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 10/017,066
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 10/001,469
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/291,118
; PRIOR FILING DATE: 2001-05-15

Mon Mar 20 08:51:26 2006

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; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-147-368B-43

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 33
US-10-533-266-2
; Sequence 2, Application US/10533266
; GENERAL INFORMATION:
; APPLICANT: FREEMAN, MATTHEW
; TITLE OF INVENTION: PROTOZOAN RHOMBROID PROTEINS
; FILE REFERENCE: MEWE-022
; CURRENT APPLICATION NUMBER: US/10/533,266
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/422,861
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic motif
US-10-533-266-2

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 34
US-10-500-264-1
; Sequence 1, Application US/10500264
; GENERAL INFORMATION:
; APPLICANT: Mahn, Andreas
; APPLICANT: Hantke, Sabine
; APPLICANT: Petsch, Dagmar
; TITLE OF INVENTION: Method of Increasing the Transgene-Coded Biomolecule Content in
; TITLE OF INVENTION: Organisms
; FILE REFERENCE: 4121-168
; CURRENT APPLICATION NUMBER: US/10/500,264
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/EP02/14512
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: EP 0 113 0319.5
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
```

```
; FEATURE:
; OTHER INFORMATION: signal polypeptide
US-10-500-264-1

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 35
US-10-189-360A-42
; Sequence 42, Application US/10189360A
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS
; TITLE OF INVENTION: AND LIGANDS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 760100.415C4
; CURRENT APPLICATION NUMBER: US/10/189,360A
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/449,249
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 08/718,904
; PRIOR FILING DATE: 1996-09-24
; PRIOR APPLICATION NUMBER: US 08/441,979
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: US 08/305,771
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 08/297,961
; PRIOR FILING DATE: 1994-08-29
; PRIOR APPLICATION NUMBER: US 08/213,446
; PRIOR FILING DATE: 1994-03-15
; PRIOR APPLICATION NUMBER: US 08/213,447
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Signal sequence in mammalian cells (cytoplasmic
; OTHER INFORMATION: translocation signal)
US-10-189-360A-42

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 1 KDEL 4

RESULT 36
US-10-428-339B-42
; Sequence 42, Application US/10428339B
; GENERAL INFORMATION:
; APPLICANT: KENWARD, Kimberly D.
; APPLICANT: SHAH, Salehzaman
; TITLE OF INVENTION: Production of Recombinant Epidermal Growth Factor in Plants
; FILE REFERENCE: 07121.0005U2
; CURRENT APPLICATION NUMBER: US/10/428,339B
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,294
; PRIOR FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for windows Version 4.0
```

; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =
US-10-428-339B-42
; OTHER INFORMATION: synthetic construct

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 37
US-11-368-804-52
; Sequence 52, Application US/11368804
; GENERAL INFORMATION:
; APPLICANT: VIRGIN, HERBERT W.
; TITLE OF INVENTION: MURINE CALICIVIRUS
; FILE REFERENCE: 56029-45752
; CURRENT APPLICATION NUMBER: US/11/368,804
; CURRENT FILING DATE: 2006-03-06
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2006-03-06
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Illustrative MNV-1 ORF1 motif
US-11-368-804-52

Query Match 100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 38
US-11-271-235-6
; Sequence 6, Application US/11271235
; GENERAL INFORMATION:
; APPLICANT: Geingross, Tillman U.
; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
; TITLE OF INVENTION: GLYCOPROTEINS
; FILE REFERENCE: GFI 100 DIV3
; CURRENT APPLICATION NUMBER: US/11/271,235
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 09/892,591
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/214,358
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/215,638
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/279,997
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Signal tetrapeptide
US-11-271-235-6

Query Match 100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 39
US-11-335-891-113
; Sequence 113, Application US/11335891
; GENERAL INFORMATION:
; APPLICANT: HALLENBECK, PAUL
; TITLE OF INVENTION: SENECA VALLEY VIRUS BASED COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 287037.127US2
; CURRENT APPLICATION NUMBER: US/11/335,891
; CURRENT FILING DATE: 2006-01-19
; PRIOR APPLICATION NUMBER: 60/506,182
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: PCT/US2004/031504
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/664,442
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/726,313
; PRIOR FILING DATE: 2005-10-13
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 113
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Seneca Valley Virus
US-11-335-891-113

Query Match 100.0%; Score 20; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 40
US-60-773-847-38
; Sequence 38, Application US/60773847
; GENERAL INFORMATION:
; APPLICANT: Syngentas Participations AG
; APPLICANT: Johnson, Brian
; APPLICANT: Chalk, Tanya
; APPLICANT: Samoylov, Vladimir
; APPLICANT: Meghji, Moez
; TITLE OF INVENTION: Corn Event 3272 and Methods of Detection Thereof
; FILE REFERENCE: 70648
; CURRENT APPLICATION NUMBER: US/60/773,847
; CURRENT FILING DATE: 2006-02-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Zea mays
US-60-773-847-38

Query Match 100.0%; Score 20; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4

Db 3 KDEL 6
|||||

RESULT 41
PCT-US04-04340-108
; Sequence 108, Application PC/TUS0404340
; GENERAL INFORMATION:
; APPLICANT: Antigenics, Inc.
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; FILE REFERENCE: 8449-405-228
; CURRENT APPLICATION NUMBER: PCT/US04/04340
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 8
; TYPE: PRT
; ORGANISM: P. falciparum
PCT-US04-04340-108

Query Match 100.0%; Score 20; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||||

Db 3 KDEL 6

RESULT 42
PCT-US04-04340-109
; Sequence 109, Application PC/TUS0404340
; GENERAL INFORMATION:
; APPLICANT: Antigenics, Inc.
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; FILE REFERENCE: 8449-405-228
; CURRENT APPLICATION NUMBER: PCT/US04/04340
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 8
; TYPE: PRT
; ORGANISM: P. falciparum
PCT-US04-04340-109

Query Match 100.0%; Score 20; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||||

Db 3 KDEL 6

RESULT 43
US-10-537-642-272
; Sequence 272, Application US/10537642
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doonan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 272
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(9)
; OTHER INFORMATION: Peptide No. 98.0257
US-10-537-642-272

Query Match 100.0%; Score 20; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
|||||

Db 5 KDEL 8

RESULT 44
PCT-US05-40707-26
; Sequence 26, Application PC/TUS0540707
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Pilkington, Glenn
; APPLICANT: Keller, Gilbert-Andre
; APPLICANT: Li, Wenlu
; APPLICANT: Burcham, Timothy S
; APPLICANT: Corral, Laura
; APPLICANT: Simon, Iris
; APPLICANT: Papkoff, Jackie
; TITLE OF INVENTION: Ovr110 Antibody Compositions and Methods of Use
; FILE REFERENCE: DEX0519W0
; CURRENT APPLICATION NUMBER: PCT/US05/40707
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/626,817
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US05-40707-26

Query Match 100.0%; Score 20; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4

```
Db      7 KDEL 10

RESULT 45
US-60-772-986-9632
; Sequence 9632, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9632
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-9632

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      4 KDEL 7

RESULT 46
US-60-772-986-14015
; Sequence 14015, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14015
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-14015

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      4 KDEL 7

RESULT 47
US-60-772-986-15264
; Sequence 15264, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15264
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-15264

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      14 KDEL 17

RESULT 48
US-60-772-986-15721
; Sequence 15721, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15721
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-15721

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      14 KDEL 17

RESULT 49
US-60-772-986-16508
; Sequence 16508, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16508
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-16508

Query Match      100.0%; Score 20; DB 8; Length 19;
```

Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
Db 14 KDEL 17

RESULT 50
US-60-772-986-16515
; Sequence 16515, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16515
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-16515

Query Match 100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
Db 14 KDEL 17

Search completed: March 20, 2006, 07:53:22
Job time : 17.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:59 ; Search time 15 Seconds
(without alignments)
25.658 Million cell updates/sec

Title: US-09-673-707-9
Perfect score: 20
Sequence: 1 KDEL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20	100.0	35	2 JX0200	gummarin - Gymnema
2	20	100.0	38	2 C60657	circumsporozoite p
3	20	100.0	38	2 B60657	circumsporozoite p
4	20	100.0	38	2 A38869	circumsporozoite p
5	20	100.0	41	2 B37188	major body fluid a
6	20	100.0	46	2 S39239	cholera enterotoxi
7	20	100.0	50	2 S19624	ornatin E - leech
8	20	100.0	50	2 AH2496	transposase asr715
9	20	100.0	52	2 S19623	ornatin C - leech
10	20	100.0	54	2 E96530	hypothetical prote
11	20	100.0	58	2 A35416	DNA topoisomerase
12	20	100.0	58	2 AD3018	conserved hypothet
13	20	100.0	60	2 AE2387	hypothetical prote
14	20	100.0	62	2 D69384	hypothetical prote
15	20	100.0	63	2 S11883	copB protein - Esc
16	20	100.0	65	2 A12513	hypothetical prote
17	20	100.0	67	2 JU0399	rflA.1 protein - p
18	20	100.0	68	2 G97737	hypothetical prote
19	20	100.0	70	2 AC2866	hypothetical prote
20	20	100.0	71	2 D81389	conserved hypothet
21	20	100.0	72	2 E81126	hypothetical prote
22	20	100.0	76	2 D84167	hypothetical prote
23	20	100.0	77	2 D69010	hypothetical prote
24	20	100.0	78	2 S69531	holin protein - ph
25	20	100.0	79	1 JN0246	calcium-binding pr
26	20	100.0	79	2 B90352	partial ORF from I
27	20	100.0	79	2 D75326	hypothetical prote
28	20	100.0	79	2 AG2544	hypothetical prote
29	20	100.0	80	2 C69204	hypothetical prote

30	20	100.0	81	2 S77318	secretory protein
31	20	100.0	82	2 JT0765	rapid lysin III pr
32	20	100.0	82	2 D64329	hypothetical prote
33	20	100.0	83	2 F82891	hypothetical prote
34	20	100.0	83	2 F82887	hypothetical prote
35	20	100.0	85	2 I40586	hypothetical prote
36	20	100.0	85	2 T39536	probable involveme
37	20	100.0	86	1 WMEC5R	replication contro
38	20	100.0	89	2 S05557	hypothetical prote
39	20	100.0	90	2 T04077	probable ribosomal
40	20	100.0	90	2 AC1030	hypothetical prote
41	20	100.0	91	2 E59100	hypothetical prote
42	20	100.0	92	2 H84264	hypothetical prote
43	20	100.0	92	2 H84296	hypothetical prote
44	20	100.0	93	2 T08319	conserved hypothet
45	20	100.0	93	2 AG2290	hypothetical prote
46	20	100.0	94	2 S60798	M protein precursor
47	20	100.0	94	2 G86415	hypothetical prote
48	20	100.0	95	2 S61076	M protein precursor
49	20	100.0	95	2 F97179	uncharacterized pr
50	20	100.0	97	1 ZCBPT9	gene 55.5 protein
51	20	100.0	99	2 S71520	M protein type 18
52	20	100.0	100	2 E90355	hypothetical prote
53	20	100.0	100	2 A99372	hypothetical prote
54	20	100.0	101	2 S74523	hypothetical prote
55	20	100.0	103	2 D64450	conserved hypothet
56	20	100.0	103	2 T40768	very hypothetical
57	20	100.0	103	2 E86853	hypothetical prote
58	20	100.0	103	2 H95245	hypothetical prote
59	20	100.0	103	2 E98110	hypothetical prote
60	20	100.0	104	2 D42721	recombination prot
61	20	100.0	105	2 E64343	hypothetical prote
62	20	100.0	105	2 B70712	hypothetical prote
63	20	100.0	106	2 C69772	thioredoxin homolo
64	20	100.0	107	2 A81595	hypothetical prote
65	20	100.0	107	2 B96906	hypothetical prote
66	20	100.0	108	2 D90051	hypothetical prote
67	20	100.0	108	2 E89993	hypothetical prote
68	20	100.0	109	2 A83265	conserved hypothet
69	20	100.0	110	1 R6SSP2	acidic ribosomal p
70	20	100.0	110	2 A96907	hypothetical prote
71	20	100.0	111	2 S10222	hypothetical prote
72	20	100.0	111	2 C90308	hypothetical prote
73	20	100.0	112	2 A64434	hypothetical prote
74	20	100.0	112	2 S75739	hypothetical prote
75	20	100.0	112	2 AH2211	hypothetical prote
76	20	100.0	113	2 G72566	hypothetical prote
77	20	100.0	114	1 JQ2242	thioredoxin h - Ar
78	20	100.0	116	1 S34611	nitrogenase (EC 1.
79	20	100.0	116	2 T10739	thioredoxin - comm
80	20	100.0	116	2 G64056	arsenate reductase
81	20	100.0	116	2 G64433	hypothetical prote
82	20	100.0	116	2 A86769	dihydroneopterin a
83	20	100.0	117	2 S75764	hypothetical prote
84	20	100.0	118	1 S34812	thioredoxin h2 - c
85	20	100.0	118	2 T10170	thioredoxin - east
86	20	100.0	118	2 I45348	V118 protein - Afr
87	20	100.0	118	2 C84181	hypothetical prote
88	20	100.0	119	2 B82782	hypothetical prote
89	20	100.0	121	1 C69190	conserved hypothet
90	20	100.0	121	2 AB2314	ferredoxin-thioeth
91	20	100.0	121	2 S18067	thyroid hormone re
92	20	100.0	121	2 T31718	hypothetical prote
93	20	100.0	121	2 T32378	hypothetical prote
94	20	100.0	121	2 S72496	transcription acti
95	20	100.0	121	2 S65809	transcription acti
96	20	100.0	121	2 S65808	transcription acti
97	20	100.0	122	2 S40152	thyroid hormone re
98	20	100.0	122	2 AB2199	hypothetical prote
99	20	100.0	122	2 B70397	hypothetical prote
100	20	100.0	123	2 JQ0368	ribosomal protein
101	20	100.0	124	2 S70043	hypothetical prote
102	20	100.0	125	2 T29941	hypothetical prote

103 20 100.0 126 2 T06861 ribosomal protein
104 20 100.0 127 1 RDAVUN ubiquinol-cytochro
105 20 100.0 127 2 A1210 glycerol-3-phospha
106 20 100.0 127 1 R3288 hypothetical prote
107 20 100.0 130 1 R3EC8 ribosomal protein
108 20 100.0 130 2 JC2280 30S ribosomal chai
109 20 100.0 130 2 AG1007 30S ribosomal subu
110 20 100.0 130 2 C91150 30S ribosomal subu
111 20 100.0 130 2 H82057 ribosomal protein
112 20 100.0 130 2 A64094 ribosomal protein
113 20 100.0 130 2 AH0027 30S ribosomal prot
114 20 100.0 130 2 A69132 ribosomal protein
115 20 100.0 132 1 JVBFFL DNA-packaging prot
116 20 100.0 132 2 E90900 probable DNA-packa
117 20 100.0 132 2 D90833 DNA packaging prot
118 20 100.0 132 2 S58123 thioredoxin (clone
119 20 100.0 133 2 H70646 hypothethical prote
120 20 100.0 133 2 H82366 conserved hypothet
121 20 100.0 133 1 J70748 FK506-binding prot
122 20 100.0 134 2 B35119 4-carboxymuconolac
123 20 100.0 134 2 C84385 hypothethical prote
124 20 100.0 135 2 S48410 ribosomal protein
125 20 100.0 135 2 D69830 hypothethical prote
126 20 100.0 136 1 B64956 flagellar protein
127 20 100.0 136 2 H90961 flagellar protein
128 20 100.0 136 2 H85809 hypothethical prote
129 20 100.0 138 1 C64005 hypothethical prote
130 20 100.0 138 2 JC6308 glia maturation fa
131 20 100.0 138 2 JC4597 signal transductio
132 20 100.0 139 2 G69543 conserved hypothet
133 20 100.0 140 2 C95277 hypothethical prote
134 20 100.0 141 1 JDBOB glia maturation fa
135 20 100.0 141 1 S22149 glia maturation fa
136 20 100.0 141 2 F72778 hypothethical prote
137 20 100.0 141 2 A96491 hypothethical prote
138 20 100.0 142 1 PT0410 hypothethical prote
139 20 100.0 144 2 E71724 hypothethical prote
140 20 100.0 144 2 A90056 aggrutin alpha cha
141 20 100.0 144 2 FC7027 hypothethical prote
142 20 100.0 145 2 F85690 hypothethical prote
143 20 100.0 145 2 S38235 mucin-like endothe
144 20 100.0 146 2 A47167 hypothethical prote
145 20 100.0 146 2 H83244 protein C28hg.1 [i
146 20 100.0 146 2 E88470 YUP8H12.12 [import
147 20 100.0 146 2 C86187 conserved hypothet
148 20 100.0 147 2 D69368 probable lipoprote
149 20 100.0 147 2 A11030
150 20 100.0 147 2

ALIGNMENTS

RESULT 1
JX0200
gurmardin - Gymnema sylvestre
N:Alternate names: sweet-taste-suppressing peptide
C:Species: Gymnema sylvestre
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C:Accession: JX0200
R:Kamei, K.; Takano, R.; Miyasaka, A.; Imoto, T.; Hara, S.
J. Biochem. 111, 109-112, 1992
A:Title: Amino acid sequence of sweet-taste-suppressing peptide (gurmardin) from the leav
A:Reference number: JX0200; MUID:92299642; PMID:1607357
A:Accession: JX0200
A:Molecule type: protein
A:Residues: 1-35 <LOC>
A:Cross-references: UNIPROT:P25810; UNIPARC:UPI000012BE09
A:Experimental source: leaf
C:Comment: This protein suppresses sweet taste.
C:Keywords: pyroglutamic acid; sweet taste
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4
|||
DB 6 KDEL 9

RESULT 2

C60657
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 7G8) (frag
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jun-2000
C:Accession: C60657
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem. Parasitol. 37, 275-280, 1989
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell
A:Reference number: A60657; MUID:90114334; PMID:2481827
A:Accession: C60657
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-38 <LOC>
A:Cross-references: UNIPARC:UPI0000177F70
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4
|||
DB 28 KDEL 31

RESULT 3

B60657
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate T9-98) (fr
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C:Accession: B60657
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem. Parasitol. 37, 275-280, 1989
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell
A:Reference number: A60657; MUID:90114334; PMID:2481827
A:Accession: B60657
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-38 <LOC>
A:Cross-references: UNIPROT:Q7M3X1; UNIPARC:UPI0000177F72
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4
|||
DB 28 KDEL 31

RESULT 4

A38869
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 427-5) (f
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C:Accession: A38869
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem. Parasitol. 37, 275-280, 1989
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell
A:Reference number: A60657; MUID:90114334; PMID:2481827
A:Accession: A38869
A:Status: preliminary; not compared with conceptual translation

RESULT 10

E96530
hypothetical protein F13F21.16 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96530
R:Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A6141; MUID:21016719; PMID:11130712
A:Accession: E96530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-54 <STO>
A:Cross-references: UNIPROT:Q9XIA7; UNIPARC:UPI00000AC31D; GB:AE005173; NID:G5430759; PI
C:Genetics:
A:Gene: F13F21.16
A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||||
DB 47 KDEL 50

RESULT 11

A35416
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.13) II - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C:Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C:Accession: A35416
R:Austin, C.A.; Barot, H.A.; Margerrison, E.E.C.; Turcatti, G.; Wingfield, P.; Hayes, M.
Biochem. Biophys. Res. Commun. 170, 763-768, 1990
A:Title: Structure and partial amino acid sequence of calf thymus DNA topoisomerase II:
A:Reference number: A35416; MUID:90343796; PMID:1696476
A:Accession: A35416
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-58 <AUS>
A:Cross-references: UNIPROT:Q7M3G2; UNIPARC:UPI000017C4F6
C:Keywords: isomerase

Query Match 100.0%; Score 20; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||||
DB 55 KDEL 58

RESULT 12

AD3018
conserved hypothetical protein Atu3752 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD3018
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD3018
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>
A:Cross-references: UNIPROT:Q8U9H6; UNIPARC:UPI00000D22FF; GB:AE008689; PIDN:AAL44562.1
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3752
A:Map position: linear chromosome

Query Match 100.0%; Score 20; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||||
DB 46 KDEL 49

RESULT 13

AE2387
hypothetical protein asr4653 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Notes: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2387
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2387
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60 <KUR>
A:Cross-references: UNIPROT:Q8YNB4; UNIPARC:UPI00000CEBDE; GB:BA000019; PIDN:BAB76352.1
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asr4653

Query Match 100.0%; Score 20; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||||
DB 52 KDEL 55

RESULT 14

D69384
hypothetical protein AF1076 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69384
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dode
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KLE>
A:Cross-references: UNIPROT:O29187; UNIPARC:UPI0000056B66; GB:AE001028; GB:AE0000782; N

Query Match 100.0%; Score 20; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||||
DB 52 KDEL 55

Query Match 100.0%; Score 20; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Query Match      100.0%; Score 20; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
```

```
Query Match      100.0%; Score 20; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
```

C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 21-Nov-1993 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C;Accession: J00399
R;Daegelen, P.; Brody, E.
Genetics 125, 237-248, 1990
A;Title: The rIIA gene of bacteriophage T4. I. Its DNA sequence and discovery
A;Reference number: PS0194; MUID:90337270; PMID:2379817

Query Match	100.0%;	Score 20;	DB 2;	Length 67;
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Query Match	100.0%;	Score 20;	DB 2;	Length 68;
Best Local Similarity	100.0%;	Pred. NO. 3.4e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

A;ACCESSION: AC2866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <KUR>

Mon Mar 20 08:51:26 2006

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Aru2357

A:Map position: circular chromosome

Query Match 100.0%; Score 20; DB 2; Length 70;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

Db 30 KDEL 33

RESULT 20

D81389 hypothetical protein Cj049c [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: D81389

C:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

R.; Parkhill, J.; M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: D81389

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-71 <PAR>

A:Cross-references: UNIPROT:Q9PI59; UNIPARC:UPI00000C3131; GB:AL1139075; GB:AL111168; NID

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj0449c

Query Match 100.0%; Score 20; DB 2; Length 71;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

Db 59 KDEL 62

RESULT 21

E81126 conserved hypothetical protein NMB1059, NMA1258 [imported] - Neisseria meningitidis (str

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: E81126; H81893

C:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: E81126

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-72 <TET>

A:Cross-references: UNIPROT:Q9JRB9; UNIPARC:UPI00000C4DEC; GB:AE002456; GB:AE002098; NID

A:Experimental source: serogroup B, strain MC58

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: H81893

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-72 <PAR>

A:Cross-references: UNIPARC:UPI00000C4DEC; GB:AL162755; GB:AL157959; NID:g7379742; PIDN:

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMB1059; NMA1258

Query Match 100.0%; Score 20; DB 2; Length 72;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

Db 59 KDEL 62

RESULT 22

D84167 hypothetical protein Vng0066h [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: D84167

R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl

Jung, K.H.; Alam, M.; Freitas, T.

proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; I

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: D84167

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-76 <STO>

A:Cross-references: UNIPROT:Q9HSU8; UNIPARC:UPI00001391DB; GB:AE004437; NID:g10579722;

C:Genetics:

A:Gene: VNG0066H

Query Match 100.0%; Score 20; DB 2; Length 76;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

Db 47 KDEL 50

RESULT 23

D69010 hypothetical protein MTH108 - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: D69010

R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, P.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fun

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: D69010

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-77 <MTH>

A:Cross-references: UNIPROT:O26211; UNIPARC:UPI0000062AA0; GB:AE000801; GB:AE000666; N

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH108

A:Start codon: TTG

Query Match 100.0%; Score 20; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

Db 37 KDEL 40

RESULT 24

holin protein - phage HP1
C;Species: phage HP1
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69531
R;Exposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scocca, Nucleic Acids Res. 24, 2360-2369, 1996
A;Title: The complete nucleotide sequence of bacteriophage HP1 DNA.
A;Reference number: S69503; MUID:96279738; PMID:8710508
A;Accession: S69531
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-78 <ESP>
A;Cross-references: UNIPROT:P51727; UNIPARC:UPI000012CAD1; EMBL:U24159; NID:g1046235; PMID:1046235
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics:
A;Gene: hol

Query Match 100.0%; Score 20; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 55 KDEL 58

RESULT 25

JN0246
calcium-binding protein, intestinal - human
N;Alternate names: calbindin D9k; ICBP
C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
C;Accession: JN0246; S24047; I56435; S21501
R;Howard, A.; Legon, S.; Spurr, N.K.; Walters, J.R.F. Biochem. Biophys. Res. Commun. 185, 663-669, 1992
A;Title: Molecular cloning and chromosomal assignment of human calbindin-D9k.
A;Reference number: JN0246; MUID:92304291; PMID:1610358
A;Accession: JN0246
A;Molecule type: mRNA
A;Residues: 1-79 <HOW>
A;Cross-references: UNIPROT:P29377; UNIPARC:UPI0000167B2D; EMBL:X65869; NID:g29601; PIDN:JN0246
A;Experimental source: intestine
R;Jeung, E.B.; Krisinger, J.; Dann, J.L.; Leung, P.C.K. FEBS Lett. 307, 224-228, 1992
A;Title: Molecular cloning of the full-length cDNA encoding the human calbindin-D(9k).
A;Reference number: S24047; MUID:92354716; PMID:1379540
A;Accession: S24047
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-79 <JEUL>
A;Cross-references: UNIPARC:UPI0000167B2D; GB:L13220; NID:g291883; PIDN:AAA35638.1; PID:R;Jeung, E.
J. Mol. Biol. 235, 1231-1238, 1994
A;Title: The human calbindin-D9k gene: complete structure and implications on rsdsteroid
A;Reference number: I56435; MUID:94141916; PMID:830886
A;Accession: I56435
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-78,'S', <JEU2>
A;Cross-references: UNIPARC:UPI000016A658; GB:L13042; NID:g291881; PIDN:AAA35637.1; PID:R;Jeung, E.
C;Comment: This protein increases calcium absorption by buffering calcium in the cytoplasm
C;Comment: This protein binds to the regulatory calmodulin binding domain of the plasma
C;Genetics:
A;Gene: GDB:CALB3
A;Cross-references: GDB:133780; OMIM:302020
A;Map position: Xp22.2-Xp22.2
A;Introns: 45/3
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; duplication; EF hand; vitamin D
F;2-79/Product: calcium-binding protein, intestinal #status predicted <MAY>
F;5-39/Domain: calmodulin repeat homology <BF1>

F;45-77/Domain: calmodulin repeat homology <BF2>

F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F;18,21,23,26,31/Binding site: calcium, low affinity (Ala, Glu, Asp, Gln, Glu) #status
F;58,60,62,64,69/Binding site: calcium, high affinity (Asp, Asn, Asp, Glu, Glu) #status

Query Match 100.0%; Score 20; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 29 KDEL 32

RESULT 26

B90352
Partial ORF from ISC1778 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90352
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chai, J.; Jang, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90352
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <KUR>
A;Cross-references: UNIPROT:Q97X69; UNIPARC:UPI00000645D2; GB:AE006641; NID:g13815141;
C;Genetics:
A;Gene: SS09135

Query Match 100.0%; Score 20; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 47 KDEL 50

RESULT 27

D75326
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75326
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75326
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <WHI>
A;Cross-references: UNIPROT:Q9RSW4; UNIPARC:UPI00000C1A40; GB:AE002038; GB:AE0000513; NID:R;White, O.
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2007
A;Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 30 KDEL 33

RESULT 28

AG2544
hypothetical protein asr7642 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2544
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 2005-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2544
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-79 <KUR>
A:Cross-references: UNIPROT:Q8ZS70; UNIPARC:UPI00000CCDCG; GB:AP003602; PIDN:BAB77285.1
C:Genetics:
A:Gene: asr7642
A:Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
DB 37 KDEL 40

RESULT 29

C69204
hypothetical protein MTH78 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C69204
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: C69204
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-80 <MTH>
A:Cross-references: UNIPROT:O26182; UNIPARC:UPI0000062C23; GB:AE000799; GB:AE000666; NID
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH78

Query Match 100.0%; Score 20; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
DB 53 KDEL 56

RESULT 30

S77318
secretory protein secE - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein ssl3335
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S77318
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77318
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-81 <KAN>
A:Cross-references: UNIPROT:P38382; UNIPARC:UPI00001357A7; EMBL:D90906; GB:AB001339; N
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: secE
A:Start codon: GTG

Query Match 100.0%; Score 20; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
DB 31 KDEL 34

RESULT 31

JT0765
rapid lysis III protein - phage T4
N:Alternate names: rIII
C:Species: phage T4
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JT0765; JU0290; S26171; JQ0526
R;Raudonikienė, A.; Nivinskas, R.
Gene 134, 135-136, 1993
A:Title: The sequences of gene rIII of bacteriophage T4 and its mutants.
A:Reference number: JT0765; MUID:94063508; PMID:8244025
A:Accession: JT0765
A:Molecule type: DNA
A:Residues: 1-82 <RAU>
A:Cross-references: UNIPROT:PI7309; UNIPARC:UPI000005CBC1
R;Raudonikienė, A.; Nivinskas, R.
Nucleic Acids Res. 18, 4280, 1990
A:Title: Nucleotide sequence of bacteriophage T4 gene 31 region.
A:Reference number: JU0290; MUID:90332452; PMID:2377483
A:Accession: JU0290
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-82 <RA2>
A:Cross-references: UNIPARC:UPI000005CBC1; EMBL:M37882; NID:9215873; PIDN:AAA32507.1; P
R;Raudonikienė, A.; Nivinskas, R.
Gene 114, 85-90, 1992
A:Title: Gene rIII is the nearest downstream neighbour of bacteriophage T4 gene 31.
A:Reference number: S26167; MUID:92267389; PMID:1587487
A:Accession: S26171
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <RA3>
A:Cross-references: UNIPARC:UPI000005CBC1; EMBL:X54536; NID:g15789; PIDN:CAA38406.1; P
R;Prilipov, A.G.; Mesyanzhinov, V.V.; Aebi, U.; Kellenberger, E.
Nucleic Acids Res. 18, 3635, 1990
A:Title: Cloning and sequencing of bacteriophage T4 genes between map positions 128.3-1
A:Reference number: JQ0524; MUID:90301484; PMID:2362813
A:Accession: JQ0526
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-63,'NLMLLHE',72,'QFVTLV' <PRI>
A:Cross-references: UNIPARC:UPI000016D7D0; EMBL:X17657; NID:g15204; PID:g15208

Query Match 100.0%; Score 20; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
|||
DB 57 KDEL 60

```

RESULT 32
D64329
hypothetical protein MJ0235 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: D64329
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64329
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-82 <BUL>
A;Cross-references: UNIPROT:Q57687; UNIPARC:UPI00001394CD; GB:U67479; GB:L77117; NID:g15
C;Genetics:
A;Map position: FOR226124-226372

Query Match 100.0%; Score 20; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 36 KDEL 39

RESULT 33
F82891
hypothetical protein UU439 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82891
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: F82891
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <GLA>
A;Cross-references: UNIPARC:UPI00000C1C69; GB:AE002140; GB:AF222894; NID:g6899420; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU439
A;Genetic code: SGC3

Query Match 100.0%; Score 20; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 32 KDEL 35

RESULT 34
E82887
hypothetical protein UU472 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82887
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: E82887
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <GLA>
A;Cross-references: UNIPARC:UPI00000C1C80; GB:AE002143; GB:AF222894; NID:g6899457; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU472
A;Genetic code: SGC3

Query Match 100.0%; Score 20; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 32 KDEL 35

RESULT 35
I40586
hypothetical protein 1 (Tn5401) - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40586
R;Baum, J.A.
J. Bacteriol. 176, 2835-2845, 1994
A;Title: Tn5401, a new class II transposable element from Bacillus thuringiensis.
A;Reference number: I40575; MUID:94245608; PMID:7514590
A;Accession: I40586
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-85 <RES>
A;Cross-references: UNIPROT:Q45701; UNIPARC:UPI00000AF7FA; EMBL:U03554; NID:g495317; P:

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 5 KDEL 8

RESULT 36
T39536
probable involvement in cytochrome oxidase assembly - fission yeast (Schizosaccharomyce
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39536
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21862
A;Accession: T39536
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-85 <WOO>
A;Cross-references: UNIPROT:O42921; UNIPARC:UPI000006B7BF; EMBL:AL021748; PIDN:CAA1686
C;Genetics:
A;Gene: SPDB:SPBC16A3.16
A;Map position: 2
A;Introns: 57/3

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 36 KDEL 39

RESULT 37
WMEC5R
replication control protein repA2 - Escherichia coli plasmid R1drrd-19
```

C;Species: Escherichia coli
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C;Accession: A04484
R;Strougaard, P.; Molin, S.; Nordstrom, K.; Hansen, F.G.
Mol. Gen. Genet. 181, 116-122, 1981
A;Title: The nucleotide sequence of the replication control region of the resistance plasmid pR101
A;Reference number: A93120; MUID:81172236; PMID:6261081
A;Accession: A04484
A;Molecule type: DNA
A;Residues: 1-86 <STO>
A;Cross-references: UNIPROT:P03855; UNIPARC:UPI00000000464
A;Note: This protein is involved in the determination of copy number in gene replication
C;Genetics:
A;Genome: plasmid
C;Superfamily: repA2 protein
C;Keywords: DNA binding; repA2 protein; plasmid copy control; plasmid replication; transcription regulation

Query Match 100.0%; Score 20; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 76 KDEL 79

RESULT 38
S05557
hypothetical protein B - phage T4
C;Species: Phage T4
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S05557
R;Hahn, S.; Rueger, W.
Nucleic Acids Res. 17, 6729, 1989
A;Title: Organization of the bacteriophage T4 genome between map positions 150.745 and 150.745
A;Reference number: S05555; MUID:89386003; PMID:2674900
A;Accession: S05557
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-89 <HAN>
A;Cross-references: UNIPROT:P13320; UNIPARC:UPI0000005CBEL; EMBL:X15818; NID:g15210; PMID:2674900

Query Match 100.0%; Score 20; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 47 KDEL 50

RESULT 39
T04077
probable ribosomal protein L9 - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04077
R;Nakamura, I.; Kameya, N.; Aoki, T.; Tada, T.; Norita, E.; Kanzaki, H.; Uchimiya, H.
submitted to the EMBL Data Library, August 1994
A;Description: Partial cDNA sequence of ribosomal protein L9 homolog from rice calli experiment
A;Reference number: Z15190
A;Accession: T04077
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-90 <NAK>
A;Cross-references: UNIPROT:P49210; UNIPARC:UPI000016DEC8; EMBL:D38012; PIDN:BAA07209.1
A;Experimental source: subsp. Japonica, callus
C;Superfamily: ribosomal protein L6/L9
C;Keywords: ribosome

Query Match 100.0%; Score 20; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 40 KDEL 43

RESULT 40
AC1030
hypothetical protein STY4564 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C;Species: Salmonella enterica subsp. enterica serovar Typhimurium
A;Note: this species has also been called Salmonella typhimurium
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC1030
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, M.; Mungall, A.; White, N.; Davies, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC1030
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <PAR>
A;Cross-references: UNIPARC:UPI000005A8A2; GB:AL513382; PIDN:CAD09340.1; PID:g16505340; C;Genetics:
A;Gene: STY4564

Query Match 100.0%; Score 20; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 13 KDEL 16

RESULT 41
E59100
hypothetical protein pX01-77 - Bacillus anthracis virulence plasmid pX01
C;Species: Bacillus anthracis
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: E59100
R;Okinkaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler, J.; Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harbored by Bacillus anthracis
A;Reference number: A59091; MUID:99445483; PMID:10515943
A;Accession: E59100
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <OKI>
A;Cross-references: UNIPROT:Q9X347; UNIPARC:UPI000000B07A1; GB:AF065404; NID:g4894216; F
A;Experimental source: strain Sterne
C;Genetics:
A;Gene: pX01-77
A;Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 19 KDEL 22

RESULT 42
H84264
hypothetical protein Vngl086c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84264
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84264
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-92 <STO>
A:Cross-references: UNIPROT:Q9HQM9; UNIPARC:UPI00000637EA; GB:AE004437; NID:gi0580634; E
C:Genetics:
A:Gene: VNG1086C

Query Match 100.0%; Score 20; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 3 KDEL 6

RESULT 43
H84296
hypothetical protein Vng1426h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84296
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-92 <STO>
A:Cross-references: UNIPROT:Q9HPX7; UNIPARC:UPI00000638AD; GB:AE004437; NID:gi0580928; E
C:Genetics:
A:Gene: VNG1426H

Query Match 100.0%; Score 20; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 27 KDEL 30

RESULT 44
T08319
conserved hypothetical protein H1232 - Halobacterium sp. (strain NRC-1) plasmid pNRC100
C:Species: Halobacterium sp.
A:Variety: strain NRC-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R:Ng, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m
A:Reference number: Z16408; MUID:99063795; PMID:9847077
A:Accession: T08319
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-93 <DAS>
A:Cross-references: UNIPROT:O52006; UNIPARC:UPI00000631EA; EMBL:AF016485; NID:g2822278;
C:Experimental source: strain NRC-1
C:Genetics:
A:Gene: HALOSP.H1232
A:Genome: plasmid pNRC100

Query Match 100.0%; Score 20; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 27 KDEL 30

RESULT 45
AG2290
hypothetical protein asr3878 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2290
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigui
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-93 <KUR>
A:Cross-references: UNIPROT:Q8YQF3; UNIPARC:UPI00000CE936; GB:BA000019; PIDN:BA075577.
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asr3878

Query Match 100.0%; Score 20; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 77 KDEL 80

RESULT 46
S60798
M protein precursor - Streptococcus pyogenes (serotype M18) (fragment)
C:Species: Streptococcus pyogenes
A:Variety: serotype M18
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60798
R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A:Title: Non-congruent relationships between variation in emm gene sequences and the p
A:Reference number: S60784; MUID:95198537; PMID:7891551
A:Accession: S60798
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-94 <WHA>
A:Cross-references: UNIPROT:Q54535; UNIPARC:UPI000017824B; EMBL:U11931
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Superfamily: M5 protein

Query Match 100.0%; Score 20; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 42 KDEL 45

RESULT 47
G86415
hypothetical protein F15D2.33 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: G86415
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ket, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86415
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <STO>
A;Cross-references: UNIPROT:Q9C7R7; UNIPARC:UPI000009D320; GB:AE005172; NID:gl0092204; F
C;Genetics:
A;Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 KDEL 4
Db 70 KDEL 73

RESULT 48
S61076
M protein precursor - Streptococcus pyogenes (serotype M30) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M30
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S61076; S60808
R;Whitmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emml gene sequences and b
A;Reference number: S61072
A;Accession: S61076
A;Molecule type: DNA
A;Residues: 1-95 <WHA>
A;Cross-references: UNIPROT:Q54547; UNIPARC:UPI0000178232; EMBL:U11944
R;Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60808
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 19-79 <WHW>
A;Cross-references: UNIPARC:UPI0000178233; EMBL:U11944
C;Genetics:
A;Gene: emm30
C;Superfamily: M5 protein
F;1-31/Domain: signal sequence (fragment) #status predicted <SIG>
F;32-95/Product: M protein (fragment) #status predicted <MAT>

Query Match 100.0%; Score 20; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 KDEL 4
Db 91 KDEL 94

RESULT 49
F97179
uncharacterized protein of YOHL family [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: F97179
R;Nolling, J.; Brecon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97179
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <KUR>
A;Cross-references: UNIPROT:Q97GU7; UNIPARC:UPI00000CA485; GB:AE001437; PIDN:AAK00225.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2268

Query Match 100.0%; Score 20; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 KDEL 4
Db 67 KDEL 70

RESULT 50
ZCBPT9
gene 55.5 protein - phage T4
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: B30292
R;Tomaschewski, J.; Rueger, W.
Nucleic Acids Res. 15, 3632-3633, 1987
A;Title: Nucleotide sequence and primary structures of gene products coded for by the T
A;Reference number: A30291; MUID:87203398; PMID:3575111
A;Accession: B30292
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: UNIPROT:P07079; UNIPARC:UPI000005CB38; GB:Y00122; NID:gl5346; PIDN
C;Genetics:
A;Gene: 55.5
C;Superfamily: phage T4 gene 55.5 protein

Query Match 100.0%; Score 20; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 KDEL 4
Db 53 KDEL 56

Search completed: March 20, 2006, 07:50:41
Job time : 19 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:50 ; Search time 147.5 Seconds
(without alignments)
19.133 Million cell updates/sec

Title: US-09-673-707-9
Perfect score: 20
Sequence: 1 KDEL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	21	2	Q5ESX0_MOUSE
2	20	100.0	26	2	Q56Z88_ARATH
3	20	100.0	28	1	ORND_PLAOR
4	20	100.0	34	2	Q41WL2_AZOVI
5	20	100.0	35	1	GUR_GYMSY
6	20	100.0	35	2	Q5S8D1_GYMSY
7	20	100.0	37	1	VPU_HVIZ8
8	20	100.0	38	2	Q7KYM2_HUMAN
9	20	100.0	38	2	Q7M3X1_PLAFA
10	20	100.0	38	2	Q7M3X5_PLAFA
11	20	100.0	38	2	Q4Z1Z5_PLABE
12	20	100.0	39	2	Q4TI99_TETNG
13	20	100.0	40	2	Q13832_HUMAN
14	20	100.0	40	2	Q13833_HUMAN
15	20	100.0	41	2	Q65527_LACFE
16	20	100.0	41	2	Q6DRV6_STRMU
17	20	100.0	41	2	Q9EQB6_MOUSE
18	20	100.0	42	2	Q9NG47_AEDAL
19	20	100.0	42	2	Q6SFQ2_9BACT
20	20	100.0	44	2	Q58N49_9CAUD
21	20	100.0	46	2	Q86KA3_DICDI
22	20	100.0	46	2	Q5SSV0_MANSW
23	20	100.0	47	2	Q81BH6_BACCR
24	20	100.0	47	2	Q5Q1L8_CRIGR
25	20	100.0	48	2	Q9UDJ7_HUMAN
26	20	100.0	49	2	Q8EB07_SHEON
27	20	100.0	50	1	ORNE_PLAOR
28	20	100.0	50	2	Q8ST38_9NEOP
29	20	100.0	50	2	Q9SVF9_DRYIU
30	20	100.0	50	2	Q50051_MYCLE
31	20	100.0	50	2	Q6RI53_STRPY

32	20	100.0	50	2	Q8YKY6_ANASP	Q8YKY6 anabaena sp
33	20	100.0	51	2	Q5VUK1_HUMAN	Q5VUK1 homo sapien
34	20	100.0	51	2	Q8T5D0_9NEOP	Q8T5D0 anartia fat
35	20	100.0	51	2	Q8T5E2_9NEOP	Q8T5E2 anartia lvt
36	20	100.0	51	2	Q95VG0_9NEOP	Q95VG0 eueidea vib
37	20	100.0	51	2	Q95VG2_9NEOP	Q95VG2 eueidea ali
38	20	100.0	52	1	ORNC_PLAOR	P25512 placobdella
39	20	100.0	52	2	Q8T5D1_9NEOP	Q8T5D1 anartia fat
40	20	100.0	52	2	Q8T5D9_9NEOP	Q8T5D9 anartia ama
41	20	100.0	52	2	Q9SPX4_PICAB	Q9SPX4 picea abies
42	20	100.0	52	2	Q65057_PICMA	Q65057 picea maria
43	20	100.0	53	2	Q8T5E1_9NEOP	Q8T5E1 anartia chr
44	20	100.0	53	2	Q30456_HORSE	Q30456 equus cabal
45	20	100.0	53	2	Q30470_HORSE	Q30470 equus cabal
46	20	100.0	53	2	Q30471_HORSE	Q30471 equus cabal
47	20	100.0	53	2	Q30476_HORSE	Q30476 equus cabal
48	20	100.0	53	2	Q9BCX3_HORSE	Q9BCX3 equus cabal
49	20	100.0	53	2	Q9SPX3_PICAB	Q9SPX3 picea abies
50	20	100.0	53	2	Q4MPAS_BACCE	Q4MPAS bacillus ce
51	20	100.0	53	2	Q8KET6_CHLTE	Q8KET6 chlorobium
52	20	100.0	54	1	TOM6_ARATH	Q9XIA7 arabidopsis
53	20	100.0	55	2	Q857F1_9CAUD	Q857F1 mycobacteri
54	20	100.0	55	2	Q4MWD1_BACCE	Q4MWD1 bacillus ce
55	20	100.0	56	2	Q9ES41_RAT	Q9ES41 rattus norv
56	20	100.0	57	2	Q7M3G2_BOVIN	Q7M3G2 bos taurus
57	20	100.0	58	2	Q8U9H6_AGR75	Q8U9H6 agrobacteri
58	20	100.0	58	2	Q81W60_BACAN	Q81W60 bacillus an
59	20	100.0	59	2	Q8T5E0_9NEOP	Q8T5E0 anartia chr
60	20	100.0	59	2	Q73FB1_BACCI	Q73FB1 bacillus ce
61	20	100.0	59	2	Q81J55_BACCR	Q81J55 bacillus ce
62	20	100.0	59	2	Q63HA5_BACC2	Q63HA5 bacillus ce
63	20	100.0	59	2	Q81VU5_BACAN	Q81VU5 bacillus an
64	20	100.0	60	1	Y4653_ANASP	Q8YKB4 anabaena sp
65	20	100.0	60	2	Q97CI2_THEVO	Q97CI2 thermoplas
66	20	100.0	60	2	Q7NSS5_CHRVO	Q7NSS5 chromobacte
67	20	100.0	61	2	Q5JH88_PYRKO	Q5JH88 pyrococcus
68	20	100.0	61	2	Q81Z37_BACAN	Q81Z37 bacillus an
69	20	100.0	61	2	Q9ADC0_STRCO	Q9ADC0 streptomyce
70	20	100.0	61	2	Q88367_MOUSE	Q88367 mus musculu
71	20	100.0	62	1	Y1076_ARCFU	Q29187 archaeoglob
72	20	100.0	62	2	Q8JH23_PPERC	Q8JH23 ostracion s
73	20	100.0	62	2	Q91801_XENLA	Q91801 xenopus lae
74	20	100.0	63	2	Q6HPS3_BACHK	Q6HPS3 bacillus th
75	20	100.0	64	1	RL29_LACPL	Q88XX8 lactobacill
76	20	100.0	64	2	Q7TBM8_POLIS	Q7TBM8 poliovirus
77	20	100.0	65	2	Q8T5D2_9NEOP	Q8T5D2 anartia fat
78	20	100.0	65	2	Q8T5D8_9NEOP	Q8T5D8 anartia ama
79	20	100.0	65	2	Q8T5E4_9NEOP	Q8T5E4 anartia ama
80	20	100.0	65	2	Q4ZP77_PSESY	Q4ZP77 pseudomonas
81	20	100.0	65	2	Q8YKK6_ANASP	Q8YKK6 anabaena sp
82	20	100.0	65	2	Q5QU38_IDILO	Q5QU38 idiomarina
83	20	100.0	66	1	RL29_BARHE	Q5G2X3 bartonella
84	20	100.0	66	1	RL29_BARQU	Q5FZD0 bartonella
85	20	100.0	66	1	RL31_GEOKA	Q5KHU0 geobacillus
86	20	100.0	66	2	Q8T5E6_9NEOP	Q8T5E6 anartia ama
87	20	100.0	66	2	Q7JQ95_BRUMA	Q7JQ95 brugia mala
88	20	100.0	66	2	Q4KH40_PSEF5	Q4KH40 pseudomonas
89	20	100.0	66	2	Q88N42_PSEPK	Q88N42 pseudomonas
90	20	100.0	67	1	Y00A_BPT4	P25186 bacterioph
91	20	100.0	67	2	Q5Z69_CRYNE	Q5Z69 cryptococcu
92	20	100.0	67	2	Q7VPH6_HAEUD	Q7VPH6 haemophilus
93	20	100.0	67	2	Q81C76_BACCR	Q81C76 bacillus ce
94	20	100.0	67	2	Q8KCB6_CHLTE	Q8KCB6 chlorobium
95	20	100.0	68	2	Q8T5E3_9NEOP	Q8T5E3 anartia lvt
96	20	100.0	68	2	Q8T5E5_9NEOP	Q8T5E5 anartia ama
97	20	100.0	68	2	Q9TMU7_ASCSU	Q9TMU7 ascaris suu
98	20	100.0	68	2	Q4YZF3_PLABE	Q4YZF3 plasmodium
99	20	100.0	68	2	Q92IW7_RICCT	Q92IW7 rickettsia
100	20	100.0	68	2	Q67546_9VIRU	Q67546 garlic comm
101	20	100.0	69	1	SSPI_BACSK	Q8WEJ3 bacillus cl
102	20	100.0	69	2	Q8MZK7_PLAFA	Q8MZK7 plasmodium
103	20	100.0	69	2	Q5CJQ6_CRYHO	Q5CJQ6 cryptospori
104	20	100.0	69	2	Q8T5D6_9NEOP	Q8T5D6 anartia ama

CC -!- FUNCTION: Potent inhibitor of fibrinogen interaction with platelet
 CC receptors expressed on glycoprotein IIB-IIIA complex. May prevent
 CC blood from clotting during either feeding and/or storage of
 CC ingested blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the ornatin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR InterPro: IPR002463; Ornatin.
 DR Pfam: PF02088; Ornatin; 1.
 DR PRINTS: PR01184; ORNATIN.
 DR ProDom: PD012062; Ornatin; 1.
 DR Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
 KW NON_TER 28 28
 FT SEQUENCE 28 AA; 3361 MW; CFC38951F91337C2 CRC64;
 SQ
 Query Match 100.0%; Score 20; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 7 KDEL 10
 RESULT 4
 Q4IWL2 AZOVI
 ID Q4IWL2 AZOVI PRELIMINARY; PRT; 34 AA.
 AC Q4IWL2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AvindRAFT_2561;
 OS Azotobacter vinelandii AvOP.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=322710;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
 RT AvOP.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Azotobacter vinelandii
 RT AvOP.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute;
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAU03000007; EAM05212.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 34 AA; 3855 MW; BAOE98F64340ABB9 CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDEL 4
 Db 26 KDEL 29
 RESULT 5
 GUR_GYMSY
 ID GUR_GYMSY STANDARD; PRT; 35 AA.
 AC P25810;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Gurmarin (Sweet-taste-suppressing peptide).
 OS Gymnema sylvestre (Gurmar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiids; Gentianales; Apocynaceae; Periplocoideae; Gymnema.
 OX NCBI_TaxID=4068;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=92299642; PubMed=1607357;
 RA Kamei K., Takano R., Miyasaka A., Imoto T., Hara S.;
 RT "Amino acid sequence of sweet-taste-suppressing peptide (gurmarin)
 RT from the leaves of *Gymnema sylvestre*.";
 RL J. Biochem. 111:109-112(1992).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95307084; PubMed=7787425;
 RA Arai K., Ishima R., Morikawa S., Miyasaka A., Imoto T., Yoshimura S.,
 RA Almoto S., Akasaka K.;
 RT "Three-dimensional structure of gurmarin, a sweet taste-suppressing
 RT polypeptide.";
 RL J. Biomol. NMR 5:297-305(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99421659; PubMed=10491100;
 RA Fletcher J.I., Dingley A.J., Smith R., Connor M., Christie M.J.,
 RA King G.F.;
 RT "High-resolution solution structure of gurmarin, a sweet-taste-
 RT suppressing plant polypeptide.";
 RL Eur. J. Biochem. 264:525-533(1999).
 CC -!- FUNCTION: Suppresses strongly the sweet taste responses in the rat
 CC with high specificity to sucrose, glucose, glycine, and saccharin.
 CC This effect is reversible, but complete recovery of the suppressed
 CC responses required at least 3h. Gurmarin showed no effect or only
 CC a very weak effect on the sweet taste sensation in humans.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR PIR: JX0200; JX0200.
 DR PDB; 1C4E; NMR; A=1-35.
 DR PDB; 1GUR; NMR; @=1-35.
 DR InterPro: IPR010485; Gurmarin.
 DR Pfam: PF06410; Gurmarin; 1.
 KW 3D-structure; Direct protein sequencing; Pyrrolidone carboxylic acid;
 KW Taste-modifying protein.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT DISULFID 3 18

reticulum and in the enhancement of virion release from the plasma membrane of infected cells.

-!- SUBCELLULAR LOCATION: Membrane-bound.

-!- MISCELLANEOUS: The Z-84 isolate was taken from a 54 year-old Zairean male.

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EMBL: J03653; AAA44683.1; -; Genomic_RNA.

DR HSP: P19554; 1VPU.

DR HIV: J03653; VPU\$JY1.

DR InterPro: IPR008187; Vpu.

DR InterPro: IPR009032; Vpu_cyt.

DR Pfam: PF00558; Vpu; 1.

KW AIDS; Transmembrane.

FT NON_TER 1

SQ SEQUENCE 37 AA; 4131 MW; 00EA53CA27D09509 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4

Db 17 KDEL 20

RESULT 8

Q7KYM2 HUMAN

ID Q7KYM2_HUMAN PRELIMINARY; PRT; 38 AA.

AC Q7KYM2;

DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Titin protein (Fragment).

GN Name-titin;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart muscle;

RX MEDLINE=95119041; PubMed=7819249;

RA Musco G., Tziatzos C., Schuck P., Pastore A.;

RT "Dissecting titin into its structural motifs: identification of an alpha helix near the N-terminus.";

RL Biochemistry 34:553-561(1995).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart muscle;

RA Label S.;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; X83270; CAA58243.1; -; mRNA.

FT NON_TER 1

FT NON_TER 38

SQ SEQUENCE 38 AA; 4562 MW; B792A11CAEE2F248 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4

Db 13 KDEL 16

RESULT 9

Q7KYM2 HUMAN

ID Q7KYM2_HUMAN PRELIMINARY; PRT; 38 AA.

AC Q7KYM2;

DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Titin protein (Fragment).

GN Name-titin;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart muscle;

RX MEDLINE=95119041; PubMed=7819249;

RA Musco G., Tziatzos C., Schuck P., Pastore A.;

RT "Dissecting titin into its structural motifs: identification of an alpha helix near the N-terminus.";

RL Biochemistry 34:553-561(1995).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart muscle;

RA Label S.;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; X83270; CAA58243.1; -; mRNA.

FT NON_TER 1

FT NON_TER 38

SQ SEQUENCE 38 AA; 4562 MW; B792A11CAEE2F248 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4

Db 13 KDEL 16

RESULT 6

Q9S8D1 GYMSY

ID Q9S8D1_GYMSY PRELIMINARY; PRT; 35 AA.

AC Q9S8D1;

DT 01-MAY-2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)

DE GURMARIN=SWEETNESS-suppressing polypeptide.

OS Gymnema sylvestre (Gurmar).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Gentianales; Apocynaceae; Periplocoideae; Gymnema.

OX NCBI_TaxID=4068;

RN [1]

RP PROTEIN SEQUENCE.

RC MEDLINE=96068945; PubMed=8534991;

RX Ota M., Ariyoshi Y.;

RT "Location of the disulfide bonds of the sweetness-suppressing polypeptide gurmarin.";

RL Biosci. Biotechnol. Biochem. 59:1956-1957(1995).

RH HSSP; P25810; IGUR.

DR InterPro: IPR010485; Gurmarin.

DR Pfam: PF06410; Gurmarin; 1.

SQ SEQUENCE 35 AA; 4233 MW; 661BCAE66E904CB6 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4

Db 6 KDEL 9

RESULT 7

VPU_HV128

ID VPU_HV128 STANDARD; PRT; 37 AA.

AC P08807;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE VPU protein (U ORF protein) (Fragment).

GN Name=VPU;

OS Human immunodeficiency virus type 1 (isolate Z-84) (HIV-1).

OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.

OC NCBI_TaxID=11681;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].

RX MEDLINE=88281278; PubMed=3395517;

RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F., Gallo R.C.;

RT "Nucleotide sequence analysis of the env gene of a new Zairian isolate of HIV-1.";

RL AIDS Res. Hum. Retroviruses 4:165-173(1988).

CC FUNCTION. Acts in the degradation of CD4 in the endoplasmic

```
O7M3X1 PLAFPA
ID O7M3X1 PLAFPA PRELIMINARY; PRT; 38 AA.
AC O7M3X1;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Circumsporozoite protein (Fragments).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=90114334; PubMed=2481827; DOI=10.1016/0166-6851(89)90159-X;
RA Lockyer M.J., Marsh K., Newbold C.I.;
RT "Wild isolates of Plasmodium falciparum show extensive polymorphism in
RT T cell epitopes of the circumsporozoite protein.";
RL Mol. Biochem. Parasitol. 37:275-280(1989).
DR PIR; B60657; B60657.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4301 MW; D51BC1C086BBD94 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4
Db 28 KDEL 31

RESULT 10
O7M3X5 PLAFPA
ID O7M3X5 PLAFPA PRELIMINARY; PRT; 38 AA.
AC O7M3X5;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Circumsporozoite protein (Fragments).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=90114334; PubMed=2481827; DOI=10.1016/0166-6851(89)90159-X;
RA Lockyer M.J., Marsh K., Newbold C.I.;
RT "Wild isolates of Plasmodium falciparum show extensive polymorphism in
RT T cell epitopes of the circumsporozoite protein.";
RL Mol. Biochem. Parasitol. 37:275-280(1989).
DR PIR; A38869; A38869.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4287 MW; CEB47BC5D6E3BD94 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4
Db 28 KDEL 31

RESULT 11
O4Z1Z5 PLABE
ID O4Z1Z5 PLABE PRELIMINARY; PRT; 38 AA.
AC O4Z1Z5;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB102634.00.0;
OS Plasmodium berghei.
```

```
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAT01001046; CAH95692.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 38
FT NON_TER 38
SQ SEQUENCE 38 AA; 4660 MW; F07E2408947C15DA CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4
Db 13 KDEL 16

RESULT 12
O4TI89 TETNG
ID O4TI89 TETNG PRELIMINARY; PRT; 39 AA.
AC O4TI89;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF2327, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0000079001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Aichouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RA Submitted (PEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01002327; CAP87393.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 39 AA; 4418 MW; E33A6CD2FA262A6B CRC64;
```

Query Match		100.0%;	Score 20;	DB 2;	Length 40;
Best Local Similarity		100.0%;	Pred. No. 1.8e+03;		
Matches		4;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 KDEL 4				
Db	23 KDEL 26				
RESULT 13					
ID	Q13832_HUMAN	PRELIMINARY;	PRT;	40 AA.	
AC	Q13832;				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	B2 bradykinin receptor basal promoter, allele BP-58-C (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=96209920; PubMed=8655154; DOI=10.1007/s004390050117;				
RA	Braun A., Maier E., Kammerer S., Mueller B., Roscher A.A.;				
RT	"A novel sequence polymorphism in the promoter region of the human				
RT	bradykinin B2-receptor gene.";				
RL	Hum. Genet. 97:688-689 (1996).				
DR	EMBL; X91663; CAA62851.1; -; Genomic DNA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
KW	Receptor.				
FT	NON TER	1			
FT	NON TER	40			
SQ	SEQUENCE	40 AA;	4140 MW;	3908E9AD371EF4A5	CRC64;
Query Match					
Best Local Similarity		100.0%;	Score 20;	DB 2;	Length 40;
Matches		4;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 KDEL 4				
Db	23 KDEL 26				
RESULT 14					
ID	Q13833_HUMAN	PRELIMINARY;	PRT;	40 AA.	
AC	Q13833;				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	B2 bradykinin receptor basal promoter, allele BP-58-T (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=96209920; PubMed=8655154; DOI=10.1007/s004390050117;				
RA	Braun A., Maier E., Kammerer S., Mueller B., Roscher A.A.;				
RT	"A novel sequence polymorphism in the promoter region of the human				
RT	bradykinin B2-receptor gene.";				
RL	Hum. Genet. 97:688-689 (1996).				
DR	EMBL; X91664; CAA62852.1; -; Genomic DNA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
KW	Receptor.				
FT	NON TER	1			
FT	NON TER	40			
SQ	SEQUENCE	40 AA;	4153 MW;	1408E9AD371EE17F	CRC64;
Query Match					
Best Local Similarity		100.0%;	Score 20;	DB 2;	Length 41;
Matches		4;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 KDEL 4				
Db	13 KDEL 16				
RESULT 16					
ID	Q8DRV6_STRMU	PRELIMINARY;	PRT;	41 AA.	
AC	Q8DRV6;				
DT	01-MAR-2003 (TrEMBLrel. 23, Created)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	Hypothetical protein SMU.2105.				
GN	OrderedLocusNames=SMU.2105;				
OS	Streptococcus mutans.				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_TaxID=1309;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=UAI59 / ATCC 700610 / Serotype C;				
RX	MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;				

RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
 RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
 RA Ferretti J.J.;
 RT "Genome sequence of *Streptococcus mutans* UA159, a cariogenic dental
 RT pathogen";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
 DR EMBL; AE015032; AAN59699.1; -; Genomic DNA.
 DR Complete proteome; Hypothetical protein.
 KW SEQUENCE 41 AA; 4849 MW; CD8F7DC062B6D60B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 5 KDEL 8

RESULT 17

Q9EQE6_MOUSE
 ID Q9EQE6_MOUSE PRELIMINARY; PRT; 41 AA.
 AC Q9EQE6_
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE General transcription factor II-I repeat domain protein 1
 DE (Fragment)
 GN Name=Gtf2lrd1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SV;
 RX MEDLINE=21250999; PubMed=11352562; DOI=10.1006/geno.2001.6507;
 RA Durkin M.E., Keck-Waggoner C.L., Popescu N.C., Thorgeirsson S.S.;
 RT "Integration of a c-myc transgene results in disruption of the mouse
 RT Gtf2lrd1 gene, the homologue of the human GTF2LRD1 gene hemizygotously
 RT deleted in Williams-Beuren syndrome.";
 RL Genomics 73:20-27 (2001).
 DR EMBL; AF257477; AAG44656.1; -; Genomic DNA.
 DR MGI; MGI:1861942; Gtf2lrd1.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0003700; F:transcription factor activity; IDA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.
 FT NON TER 41
 SQ SEQUENCE 41 AA; 4482 MW; D7E29ECA570059DC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 27 KDEL 30

RESULT 18

Q9NG47_AEDAL
 ID Q9NG47_AEDAL PRELIMINARY; PRT; 42 AA.
 AC Q9NG47;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal S5 protein (Fragment).
 OS Aedes albopictus (Forest day mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Culicinae; Culicini; Aedes; Stegomyia.

OX NCBI_TaxID=71160;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yang F.F., Zhao T.T., Li D.D.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF263471; AAF73440.1; -; mRNA.
 DR GO; GO:0015935; C:small ribosomal subunit; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR InterPro; IPR005716; Ribosomal_S7e/a.
 DR Pfam; PF00177; Ribosomal_S7; 1.
 DR TIGRFAMs; TIGR01028; S7_S5_E_A; 1.
 FT NON TER 1
 SQ SEQUENCE 42 AA; 4711 MW; CE1FB5123B5053A2 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 31 KDEL 34

RESULT 19

Q6SFQ2_9BACT
 ID Q6SFQ2_9BACT PRELIMINARY; PRT; 42 AA.
 AC Q6SFQ2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 DE ORFNames=BBAC000-36A07.5;
 GN uncultured bacterium 580.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=257400;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA DeLong E.F.;
 RT "Monterey Bay Coastal Ocean Microbial Observatory environmental clone
 RT sequencing.";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY458647; AAR38160.1; -; Genomic DNA.
 KW Hypothetical protein.
 FT NON TER 41
 SQ SEQUENCE 42 AA; 5136 MW; 26A3A4736779A936 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
 ||||
 Db 24 KDEL 27

RESULT 20

Q58N49_9CAUD
 ID Q58N49_9CAUD PRELIMINARY; PRT; 44 AA.
 AC Q58N49;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PPSP7_009;
 OS Cyanophage P-SSP7.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
 OX NCBI_TaxID=268748;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
RX PubMed=15828858; DOI=10.1371/journal.pbio.0030144;
RA Sullivan M.B., Coleman M.L., Weigle P., Rohwer F., Chisholm S.W.;
RT "Three prochlorococcus cyanophage genomes: signature features and
ecological interpretations."; PLoS Biol. 3:E144-E144(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindell D., Sullivan M.B., Johnson Z.I., Tolonen A.C., Rohwer F.,
RA Chisholm S.W.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY939843; AAX44189.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 44 AA; 5189 MW; 57C219AD9FAFD4F7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 28+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 23 KDEL 26

RESULT 21
Q86KA3_DICDI PRELIMINARY; PRT; 46 AA.
AC Q86KA3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80167608;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugeng R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lounsgood H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauly G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";

RL Nature 0:0-0(2005).
DR EMBL; AC116956; AAO51164.1; -; Genomic_DNA.
DR EMBL; AAF10100027; EAL70094.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 46 AA; 5295 MW; 90B4DD2FFD66E424 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 26 KDEL 29

RESULT 22
Q65SV0_MNSM PRELIMINARY; PRT; 46 AA.
AC Q65SV0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=MS1353;
OS Mannheimia succiniciproducens (strain MBEL55E). Pasteurellales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt101010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens."; Nat. Biotechnol. 22:1275-1281(2004).
RN Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AE016827; AAU37960.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 46 AA; 5633 MW; 08EF7F4B232074B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 9 KDEL 12

RESULT 23
Q81BH6_BACCR PRELIMINARY; PRT; 47 AA.
AC Q81BH6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BC3181;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis."; Nature 423:87-91(2003).
RL Nature 423:87-91(2003).

DR EMBL; AE017008; AAP10123.1; -; Genomic_DNA.
 DR InterPro; IPR006542; Cons_hypoth1655.
 DR Pfam; PF06486; DUF1093; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 47 AA; 5565 MW; D36072B5A6AFA0A4 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 Db 33 KDEL 36

RESULT 24

Q5Q1L8 CRIGR PRELIMINARY; PRT; 47 AA.

AC Q5Q1L8; DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Putative ER-resident protein ERdj5 (Fragment).
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetinae; Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Chen P., Harcum S.W.;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY788841; AAV69868.1; -; mRNA.
 DR InterPro; IPR000886; ER target S.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 47 AA; 5607 MW; C3DBF0A6325A21E1 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 Db 44 KDEL 47

RESULT 25

Q9UDJ7 HUMAN PRELIMINARY; PRT; 48 AA.

AC Q9UDJ7; DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 26, Last annotation update)
 DE Nucleolar shuttle protein B-23=38 kDa major NOS-binding protein (Fragments).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA MEDLINE=93300776; PubMed=8314759;
 RX Adachi Y., Copeland T.D., Hatanaka M., Oroszlan S.;
 RT "Nucleolar targeting signal of Rex protein of human T-cell leukemia virus type I specifically binds to nucleolar shuttle protein B-23.";
 RL J. Biol. Chem. 268:13930-13934 (1993).
 FT NON_TER 1
 FT NON_CONS 18 19
 FT NON_CONS 33 34
 FT NON_TER 48 48
 SQ SEQUENCE 48 AA; 4783 MW; 5D73D533BD386A9E CRC64;

Query Match 100.0%; Score 20; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 Db 5 KDEL 8

RESULT 26

Q8EB07 SHEON PRELIMINARY; PRT; 49 AA.

AC Q8EB07; DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein SO3729.
 GN OrderedLocustNames=SO3729;
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Shewanellaceae; Shewanella.
 OX NCBI_TaxID=70863;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MR-1;
 RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.D., Methe B.A.,
 RA Clayton R.A., Meyer T., Tsaplin A., Scott J., Beanan M.J.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
 RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
 RA Venter J.C., Neillson K.H., Fraser C.M.;
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis.";
 RL Nat. Biotechnol. 20:1118-1123 (2002).
 DR EMBL; AE015806; AAN56713.1; -; Genomic_DNA.
 DR TIGR; SO3729; -.
 KW Complete proteome.

SQ SEQUENCE 49 AA; 5340 MW; 7ABE848EAD0FFA80 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
 Db 31 KDEL 34

RESULT 27

ORNE PLAOR STANDARD; PRT; 50 AA.

AC P25514; DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ornatin E.
 OS Placobdella ornata (Turtle leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Placobdella.
 OX NCBI_TaxID=6415;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92111479; PubMed=1765068;
 RA Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;
 RT "Ornatin: potent glycoprotein fib-fib antagonists and platelet
 RT aggregation inhibitors from the leech Placobdella ornata.";
 RL Eur. J. Biochem. 202:1073-1082 (1991).
 CC -!- FUNCTION: Potent inhibitor of fibrinogen interaction with platelet

BEST LOCAL SIMILARITY	100.0%	FREQ. NO:	2.58+05;
MATCHES	4:	CONSERVATIVE	0:
MISMATCHES	0:	MISMATCHES	0:
INDELS	0:	INDELS	0:
GAPS	0:	GAPS	0:

RN [1]

OX NCBI TaxID=1769;

Best Local Similarity 100.0%; PRed: NO. 2.3e+05;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15182; AAA62266.1; -; Genomic_DNA.
SQ SEQUENCE 50 AA; 5563 MW; 5B5A4419AD5DD6C2 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 41 KDEL 44

RESULT 31
Q6RI53 STRPY PRELIMINARY; PRT; 50 AA.
AC Q6RI53;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15071004; DOI=10.1126/JCM.42.4.1559-1563.2004;
RA Hasenbein M.E., Warner J.E., Lambert K.G., Cole S.E., Onderdonk A.B.,
RA McAdam A.J.;
RT "Detection of multiple macrolide- and lincosamide-resistant strains of
RT Streptococcus pyogenes from patients in the Boston area."
RL J. Clin. Microbiol. 42:1559-1563(2004).
DR EMBL; AY497033; AAR89487.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5828 MW; F3F49D82A58B8FDC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 11 KDEL 14

RESULT 32
Q8YKY6 ANASP
ID Q8YKY6 ANASP PRELIMINARY; PRT; 50 AA.
AC Q8YKY6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transposase.
GN OrderedLocustNames=asr7152;
OS Anabaena sp. (strain PCC 7120).
OG Plasmid pCC7120alphi.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RL cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; BA000020; BAB78236.1; -; Genomic_DNA.
DR PIR; AH2496; AH2496.
SQ Complete proteome; Plasmid.
KW SEQUENCE 50 AA; 5761 MW; EE163ACA7E5C489B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 8 KDEL 11

RESULT 33
Q5VUK1 HUMAN PRELIMINARY; PRT; 51 AA.
AC Q5VUK1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein (Fragment).
GN Name=RP11-290P14.1; ORFNames=RP11-290P14.1-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Peck A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL589763; CAH72046.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 51 AA; 5737 MW; 9D2FB367916CE45A CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 21 KDEL 24

RESULT 34
Q8TSD0 9NEOP
ID Q8TSD0 9NEOP PRELIMINARY; PRT; 51 AA.
AC Q8TSD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 24, Last annotation update)
DE Triosephosphate isomerase (Fragment).
OS Anartia fatima.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX NCBI_TaxID=145889;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
RA Blum M.J., Birmingham E., Dagmahapatra K.;
RT "A molecular phylogeny of the neotropical butterfly genus Anartia
RT (Lepidoptera: Nymphalidae)."
RL Mol. Phylogenet. Evol. 26:46-55(2003).
DR EMBL; AY038691; AAM03323.1; -; Genomic_DNA.
DR HSSP; P00940; ITPH.
DR SKR; Q8TSD0; 1-48.
DR GO; GO:0016853; F:isomerase activity; IEA.

DR GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000652; Triophos_ismrse.
DR Pfam: PF00121; TIM; 1.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5523 MW; E1E59B6F54436BAF CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db |||||
3 KDEL 6

RESULT 35
Q8T5E2_9NEOP
ID Q8T5E2_9NEOP PRELIMINARY; PRT; 51 AA.
AC Q8T5E2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Triosephosphate isomerase (Fragment).
OS Anartia lytrea.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX NCBI_TaxID=165847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
BLUM M.J., Bermingham E., Dasmahapatra K.;
RT "A molecular phylogeny of the neotropical butterfly genus Anartia
(Lepidoptera: Nymphalidae).";
RL Mol. Phylogenet. Evol. 26:46-55 (2003).
DR EMBL: AY038677; AAM03325.1; -; Genomic_DNA.
DR HSSP: P00940; 1TPH.
DR SMR: Q8T5E2; 2-46.
DR GO:0016853; F:isomerase activity; IEA.
DR GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000652; Triophos_ismrse.
DR Pfam: PF00121; TIM; 1.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5531 MW; 55D759F281E4EEA CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db |||||
1 KDEL 4

RESULT 36
Q95VG0_9NEOP
ID Q95VG0_9NEOP PRELIMINARY; PRT; 51 AA.
AC Q95VG0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Triosephosphate isomerase (Fragment).
OS Name=Tpi;
GN Eueides vibilia.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Eueides.

OX NCBI_TaxID=101930;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337200; PubMed=12446809;
RA Beltran M., Jiggins C.D., Bull V., Linares M., Mallet J.,
RA McMillan W.O., Bermingham E.;
RT "Phylogenetic discordance at the species boundary: comparative gene
genealogies among rapidly radiating heliconius butterflies.";
RL Mol. Biol. Evol. 19:2176-2190(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Beltran M.S., Jiggins C.D., Bull V., McMillan O., Bermingham E.,
RA Mallet J., Linares M.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF413796; AAL08557.1; -; Genomic_DNA.
DR HSSP: P00940; 1TPH.
DR SMR: Q95VG0; 1-48.
DR GO:0016853; F:isomerase activity; IEA.
DR GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000652; Triophos_ismrse.
DR Pfam: PF00121; TIM; 1.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5523 MW; F98584DEFF436BAF CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db |||||
3 KDEL 6

RESULT 37
Q95VG2_9NEOP
ID Q95VG2_9NEOP PRELIMINARY; PRT; 51 AA.
AC Q95VG2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Triosephosphate isomerase (Fragment).
GN Name=Tpi;
OS Eueides aliphera.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Eueides.
OX NCBI_TaxID=33449;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337200; PubMed=12446809;
RA Beltran M., Jiggins C.D., Bull V., Linares M., Mallet J.,
RA McMillan W.O., Bermingham E.;
RT "Phylogenetic discordance at the species boundary: comparative gene
genealogies among rapidly radiating heliconius butterflies.";
RL Mol. Biol. Evol. 19:2176-2190(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Beltran M.S., Jiggins C.D., Bull V., McMillan O., Bermingham E.,
RA Mallet J., Linares M.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF413794; AAL08555.1; -; Genomic_DNA.
DR HSSP: P00940; 1TPH.
DR SMR: Q95VG2; 1-48.
DR GO:0016853; F:isomerase activity; IEA.
DR GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000652; Triophos_ismrse.
DR Pfam: PF00121; TIM; 1.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 51 51

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FT  NON TER      51      51
SQ  SEQUENCE 51 AA; 5509 MW;  F9815FFEFF436BAF  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  3 KDEL 6

RESULT 38
ORNC PLAOR
ID  ORNC PLAOR      STANDARD;      PRT;      52 AA.
AC  P25512;
DT  01-MAY-1992 (Rel. 22, Created)
DT  01-MAY-1992 (Rel. 22, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Ornatin C.
OS  Placobdella ornata (Turtle leech).
OC  Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC  Rhynchobdellida; Glossiphoniidae; Placobdella.
OX  NCBI_TaxID=6415;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=92111479; PubMed=1765068;
RA  Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;
RT  "Ornatins: potent glycoprotein IIB-IIIa antagonists and platelet
RL  Eur. J. Biochem. 202:1073-1082(1991).
CC  -!- FUNCTION: Potent inhibitor of fibrinogen interaction with platelet
CC  receptors expressed on glycoprotein IIB-IIIa complex. May prevent
CC  blood from clotting during either feeding and/or storage of
CC  ingested blood.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the ornatin family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  PIR; S19623;
DR  InterPro: IPR002463; Ornatin.
DR  Pfam; PF02088; Ornatin; 1.
DR  PRINTS; PR01184; ORNATIN.
DR  ProDom; PD012062; Ornatin; 1.
DR  KX  Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
FW  MOTIF 42 44 Cell attachment site.
SQ  SEQUENCE 52 AA; 5845 MW;  BA55CA7408EF4F09  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  7 KDEL 10

RESULT 39
Q8T5D1_9NEOP
ID  Q8T5D1_9NEOP PRELIMINARY;      PRT;      52 AA.
AC  Q8T5D1;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Triosephosphate isomerase (Fragment).
OS  Anartia fatima.
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

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OC  Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX  NCBI_TaxID=145889;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
RA  Blum M.J., Birmingham E., Dasmahapatra K.;
RT  "A molecular phylogeny of the neotropical butterfly genus Anartia
RL  (Lepidoptera: Nymphalidae).";
RL  Mol. Phylogenet. Evol. 26:46-55(2003).
DR  EMBL; AY038690; AAM03322.1; -; Genomic_DNA.
DR  HSSP; P00940; ITPH.
DR  SMR; Q8T5D1; 2-49.
DR  GO; GO:0016853; F:isomerase activity; IEA.
DR  GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro: IPR000652; Triophos_ismrse.
DR  Pfam; PF00121; TIM; 1.
KW  isomerase.
FT  NON TER      1      1
FT  NON TER      52     52
SQ  SEQUENCE 52 AA; 5620 MW;  F9859E17CF2EA5EF  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  4 KDEL 7

RESULT 40
Q8T5D9_9NEOP
ID  Q8T5D9_9NEOP PRELIMINARY;      PRT;      52 AA.
AC  Q8T5D9;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Triosephosphate isomerase (Fragment).
OS  Anartia amatheia.
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC  Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX  NCBI_TaxID=145890;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
RA  Blum M.J., Birmingham E., Dasmahapatra K.;
RT  "A molecular phylogeny of the neotropical butterfly genus Anartia
RL  (Lepidoptera: Nymphalidae).";
RL  Mol. Phylogenet. Evol. 26:46-55(2003).
DR  EMBL; AY038680; AAM03328.1; -; Genomic_DNA.
DR  HSSP; P00940; ITPH.
DR  SMR; Q8T5D9; 1-48.
DR  GO; GO:0016853; F:isomerase activity; IEA.
DR  GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro: IPR000652; Triophos_ismrse.
DR  Pfam; PF00121; TIM; 1.
KW  isomerase.
FT  NON TER      1      1
FT  NON TER      52     52
SQ  SEQUENCE 52 AA; 5620 MW;  8759859E6F54436B  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  3 KDEL 6

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RESULT 41
QSPX4 PICAB
ID QSPX4_PICAB PRELIMINARY; PRT; 52 AA.
AC QSPX4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative 60S ribosomal protein L31 (Fragment).
OS Name=Sb42;
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99436016; PubMed=10504420;
RA Perry D.J., Isabel N., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and
RT nature of variation revealed in norway spruce.";
RL Heredity 83:239-248(1999);
DR EMBL; AF127445; AAF02462.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000054; Ribosomal_L31e.
DR Pfam; PF01198; Ribosomal_L31e; 1.
KW Ribosomal protein.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 52 AA; 5968 MW; 76842A0D745F72D7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 23 KDEL 26

RESULT 42
O65057 PICMA
ID O65057_PICMA PRELIMINARY; PRT; 52 AA.
AC O65057;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ER-targeted protein (Fragment).
GN Name=Sb19;
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98278823; PubMed=9611216;
RA Perry D.J., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: development,
RT characterization and analysis of linkage in black spruce.";
RL Genetics 149:1089-1098(1998).
DR EMBL; AF012125; AAC32119.1; -; mRNA.
DR InterPro; IPR000886; ER_target_S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 52 AA; 6012 MW; A3AFB2C63F8B4791 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 49 KDEL 52

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RESULT 43
OBTSE1_9NEOP
ID OBTSE1_9NEOP PRELIMINARY; PRT; 53 AA.
AC OBTSE1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Triosephosphate isomerase (Fragment).
OS Anartia chrysopoelea.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX NCBI_TaxID=165849;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
RA Blum M.J., Bermingham E., Dasmahapatra K.;
RT "A molecular phylogeny of the neotropical butterfly genus Anartia
RT (Lepidoptera: Nymphalidae).";
RL Mol. Phylogenet. Evol. 26:46-55(2003).
DR EMBL; AX038678; AAM03326.1; -; Genomic_DNA.
DR HSP; P00940; ITPH.
DR SMR; OBTSE1; 1-48.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000652; Triophos_iamrae.
DR Pfam; PF00121; TIM; 1.
KW isomerase.
FT NON TER 1
FT NON TER 53
FT NON TER 53
SQ SEQUENCE 53 AA; 5718 MW; 22D759859B5F5443 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 3 KDEL 6

RESULT 44
Q30456 HORSE
ID Q30456_HORSE PRELIMINARY; PRT; 53 AA.
AC Q30456;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC EIA-DQbeta cell surface glycoprotein (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Blood.
RX MEDLINE=93370708; PubMed=8363103;
RA Szalai G., Bailey E., Gerber H., Lazary S.;
RT "DNA sequence analysis of serologically detected ELA class II
RT haplotypes at the equine DQ beta locus.";
RL Anim. Genet. 24:187-190(1993).
DR EMBL; L08739; AAA30933.1; -; Genomic_DNA.
DR SMR; Q30456; 1-53.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.

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DR Pfam; PF00969; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON TER 1 53
FT NON TER 53 53
SQ SEQUENCE 53 AA; 6341 MW; 88884EF9415FC6E3 CRC64;

Query Match      100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 45 KDEL 48

RESULT 45
Q30470 HORSE
ID Q30470 HORSE PRELIMINARY; PRT; 53 AA.
AC Q30470;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC ELA-DQbeta cell surface glycoprotein (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Szalai G., Bailey E., Gerber H., Lazary S.;
RT "DNA sequence analysis of serologically detected ELA class II
haplotypes at the equine DQ beta locus."
RL Anim. Genet. 24:187-190(1993).
DR EMBL; L08740; AAA30935.1; -; Genomic_DNA.
DR SMR; Q30470; 1-53.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON TER 1 53
FT NON TER 53 53
SQ SEQUENCE 53 AA; 6266 MW; 88885ABA615FC6E3 CRC64;

Query Match      100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 45 KDEL 48

RESULT 47
Q30476 HORSE
ID Q30476 HORSE PRELIMINARY; PRT; 53 AA.
AC Q30476;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC ELA-DQbeta cell surface glycoprotein (fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Szalai G., Bailey E., Gerber H., Lazary S.;
RT "DNA sequence analysis of serologically detected ELA class II
haplotypes at the equine DQ beta locus."
RL Anim. Genet. 24:187-190(1993).
DR EMBL; L08747; AAA30941.1; -; Genomic_DNA.
DR SMR; Q30476; 1-53.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON TER 1 53
FT NON TER 53 53
SQ SEQUENCE 53 AA; 6309 MW; 88885AA9415FC6E3 CRC64;

Query Match      100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 45 KDEL 48

RESULT 46
Q30471 HORSE
ID Q30471 HORSE PRELIMINARY; PRT; 53 AA.
AC Q30471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC ELA-DQbeta cell surface glycoprotein (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;

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DR GO: 0006412; P:protein biosynthesis; IEA.
DR InterPro: IPR00054; Ribosomal_L3le.
DR Pfam: PF01198; Ribosomal_L3le; 1.
KW Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 53 AA; 6025 MW; 01842A0D00B9A9CE CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 24 KDEL 27

RESULT 50
Q4MPA5_BACCE
ID Q4MPA5_BACCE PRELIMINARY; PRT; 53 AA.
AC Q4MPA5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Alpha/beta hydrolase.
ORFNames=BCE_G9241.2817;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEK01000019; EAL14002.1; -; Genomic_DNA.
KW Hydrolase.
SQ SEQUENCE 53 AA; 6525 MW; DD5B74F6551F7970 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 5 KDEL 8

Search completed: March 20, 2006, 07:57:21
Job time : 154.5 secs

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QY 1 KDEL 4
DB 45 KDEL 48

RESULT 48
Q9BCX3_HORSE
ID Q9BCX3_HORSE PRELIMINARY; PRT; 53 AA.
AC Q9BCX3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=ELA-DOB;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactylia; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22027051; PubMed=12030922;
RA Horin P., Matiasovic J.;
RT "A second locus and new alleles in the major histocompatibility
RT complex class II (ELA-DOB) region in the horse.";
RL Anim. Genet. 33:195-200(2002).
DR EMBL; AF348966; AAK29638.1; -; mRNA.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0045012; F:MHC class II receptor activity; IEA.
DR GO: 0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO: 0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO: 0006955; P:immune response; IEA.
DR InterPro: IPR000353; MHC_II_beta_N.
DR Pfam: PF00969; MHC_II_beta_1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 6380 MW; 8EDCC47AE79061B7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 45 KDEL 48

RESULT 49
Q9SPX3_PICAB
ID Q9SPX3_PICAB PRELIMINARY; PRT; 53 AA.
AC Q9SPX3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative 60S ribosomal protein L31 (Fragment).
GN Name=Sb42;
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=99436016; PubMed=10504420;
RA Perry D.J., Isabel N., Bouquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and
RT nature of variation revealed in norway spruce.";
RL Heredity 83:239-248(1999).
DR EMBL; AF127446; AAF02463.1; -; Genomic_DNA.
DR GO: 0005622; C:intracellular; IEA.
DR GO: 0005840; C:ribosome; IEA.
DR GO: 0003735; F:structural constituent of ribosome; IEA.

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